

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	Alignments
Searched:	1612378 seqs, 512079187 residues		
Total number of hits satisfying chosen parameters:	1612378		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *		
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	
Run on:	July 1, 2005, 18:05:25 ;	Search time 109.109 Seconds (without alignments)	
Title:	US-09-591-632-2		
Perfect score:	3594		
Sequence:	1 MSDSNQGNQNQNYQQYSQNG. FTLRDQGTTIAIGKIVKIAE 685		
RESULT 1	BRF2_YEAST	STANDARD:	
ID	BRF2_YEAST	PRT:	685 AA.
AC	P05453; P05420;	PRTR:	
DT	01-NOV-1988 (Rel. 09, Created)	PRTR:	
DT	01-NOV-1988 (Rel. 09, Last sequence update)	PRTR:	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	PRTR:	
DE	Eukaryotic peptide chain release factor Grp-binding subunit (ERF2) (Transl. release factor 3) (ERF3) (Omnipotential suppressor protein 2) (G1 to S phase transition protein 1).	PRTR:	
GN	Name-SUP35; Synonyms-GST1, PNM2, SAL3, SUP12, SUP2;	PRTR:	
GN	OrderedLocusNames-YDR174W; ORFNNames-YD995.05;	PRTR:	
OS	Saccharomyces cerevisiae (Baker's Yeast).	PRTR:	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyces; Saccharomycetaceae; Saccharomyces.	PRTR:	
OC	NCBI_TaxID=4932;	PRTR:	
RN		PRTR:	
RX	SEQUENCE FROM N.A. MEDLINE=863229727; PubMed=3047009; DOI=10.1016/0378-1119(88)90223-5;	PRTR:	
RA	Kushnirov V.V., Ter-Avanesyan M.D., Telickov M.V., Surguchov A.P., [1]	PRTR:	
RA	"Nucleotide sequence of the SUP2 (SUP35) gene of Saccharomyces cerevisiae." Gene 66:45-54 (1988).	PRTR:	
RL	T2	PRTR:	
RN	SEQUENCE FROM N.A. MEDLINE=87219095; PubMed=3556015; DOI=10.1016/0014-5793(87)80157-6;	PRTR:	
RX	Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirnov V.N., Ing-vechtomov S.G., [2]	PRTR:	
RA	"SUP2 suppressor protein of yeast." A fusion protein related to the elongation factors." FEBS Lett. 215:257-260(1987).	PRTR:	
RT	"Localization of possible functional domains in sup2 gene product of the yeast Saccharomyces cerevisiae." FEBS Lett. 215:257-260(1987).	PRTR:	
RL	[3]	PRTR:	
RN	SEQUENCE FROM N.A. MEDLINE=88172303; PubMed=3280807;	PRTR:	
RX	Wilson P.G., Culbertson M.R., [4]	PRTR:	
RA	"SUP12 suppressor protein of yeast." A fusion protein related to the elongation factors." FEBS Lett. 215:257-260(1987).	PRTR:	
RT	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain." J. Mol. Biol. 199:539-573(1988);	PRTR:	
RT	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain." J. Mol. Biol. 199:539-573(1988);	PRTR:	
RL	[5]	PRTR:	
RN	SEQUENCE FROM N.A. MEDLINE=88296422; PubMed=2841115;	PRTR:	
RX	Kukuchi Y., Shimatake H., Kikuchi A.; RA	PRTR:	
RT	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain." J. Mol. Biol. 199:539-573(1988);	PRTR:	
RT	"A yeast gene required for the G1-to-S transition encodes a protein containing an A-kinase target site and GTPase domain." J. Mol. Biol. 199:539-573(1988);	PRTR:	
RL	[6]	PRTR:	
RN	SEQUENCE FROM N.A. MEDLINE=97313263; PubMed=9169867;	PRTR:	
RX	Jacq C., Alt-Moerle J., Andre B., Arnold W., Bahr A., Ballesta J.P.G., Bargeon M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C., Boskovic J., Brandt P., Brueckner M.J., Buitrago M.J., Coster F., Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M., [7]	PRTR:	

RA	FT DOMAIN 139	249	Charged.
RA	FT NP-BIND 267	274	GTP (By similarity).
RA	FT NP-BIND 344	348	GTP (By similarity).
RA	FT NP-BIND 406	409	GTP (By similarity).
RA	FT SITE 273	273	Interacts with GTP/GDP (By similarity).
RA	FT SITE 407	407	Interacts with GTP/GDP (By similarity).
RA	FT MOD-RES 341	341	Phosphothreonine (By similarity).
RA	FT CONFLICT 53	53	S -> C (in Ref. 4).
RA	SQ SEQUENCE 685 AA;	76551 MW;	43912A67DFA153 CRC64;
RA	Query Match 100.0%;	Score 3594;	DB 1; Length 685;
RA	Best Local Similarity 100.0%;	Pred. No. 2 9e-175;	
RA	Matches 685; Conservative 0;	MMatches 0;	Indels 0;
RA	RA GapS 0;		
RA	Qy 1 MSDSNGNNQNYQQYSONGNQOOGNNRQGYQAYNAQAQPAGGYQYQNYQGSGYQGQGY 60		
RA	Db 1 MSDSNGNNQNYQQYSONGNQOOGNNRQGYQAYNAQAQPAGGYQYQNYQGSGYQGQGY 60		
RA	Qy 61 QQYNPDAGYQQYNPQGGYQQYQOFNPQGRGNYKFNFNNNLOGYQAGFQPO 120		
RA	Db 61 QQYNPDAGYQQYNPQGGYQQYQOFNPQGRGNYKFNFNNNLOGYQAGFQPO 120		
RA	Qy 121 SQGMSLNDFQKQQAAPKPKTLKLVSSSGTKLAPKESDKKEEKSAETK 180		
RA	Db 121 SQGMSLNDFQKQQAAPKPKTLKLVSSSGTKLAPKESDKKEEKSAETK 180		
RA	Qy 181 EPTKEPTKVEEPVKKEEKPVQTEEEKTEKSLPKVEDIKLSESTHTNNNANTASADALIK 240		
RA	Db 181 EPTKEPTKVEEPVKKEEKPVQTEEEKTEKSLPKVEDIKLSESTHTNNNANTASADALIK 240		
RA	Qy 241 EQEEETDDEVNDMFGKDKAVSLLIYHVGDAKSTMGNLILYLTGSVYDKRTEKVERAK 300		
RA	Db 241 EQEEETDDEVNDMFGKDKAVSLLIYHVGDAKSTMGNLILYLTGSVYDKRTEKVERAK 300		
RA	Qy 301 DAGRGWYLISWMDTNKEERNDGKTLVEGVKAYFEETKRRYTLIDAPGHKMTVSEMGAS 360		
RA	Db 301 DAGRGWYLISWMDTNKEERNDGKTLVEGVKAYFEETKRRYTLIDAPGHKMTVSEMGAS 360		
RA	Qy 361 QADVGVLVISARKGEYETGPERGGTREHALAKTQGVNKVNVVNMKDDPTVNSKERY 420		
RA	Db 361 QADVGVLVISARKGEYETGPERGGTREHALAKTQGVNKVNVVNMKDDPTVNSKERY 420		
RA	Qy 421 DQCVSNVSNFNLRAIGYNIKTDVVFPMVSGYSGANLKDHDVDPKECPWYTGPTILEYDDTMN 480		
RA	Db 421 DQCVSNVSNFNLRAIGYNIKTDVVFPMVSGYSGANLKDHDVDPKECPWYTGPTILEYDDTMN 480		
RA	Qy 481 HVDRHINAPMLPIAKMKGDLGTVIYEGKIESGHIIKGQSTLJMPNTAVELQNYNETEN 540		
RA	Db 481 HVDRHINAPMLPIAKMKGDLGTVIYEGKIESGHIIKGQSTLJMPNTAVELQNYNETEN 540		
RA	Qy 541 EVDMAMCGEQYKLRIKGVEEDISPFVLTSPKNPIKSUTKFKVQAQIAIVELKSIAAGFS 600		
RA	Db 541 EVDMAMCGEQYKLRIKGVEEDISPFVLTSPKNPIKSUTKFKVQAQIAIVELKSIAAGFS 600		
RA	Qy 601 CVMHHTAEEVHKLHLEKGTMTRSKKPPAFAKGMKVIAVLETEAPVCVETYQDY 660		
RA	Db 601 CVMHHTAEEVHKLHLEKGTMTRSKKPPAFAKGMKVIAVLETEAPVCVETYQDY 660		
RA	Qy 661 PQLGRTLDRDGTTIAIGKIVKIAE 685		
RA	Db 661 PQLGRTLDRDGTTIAIGKIVKIAE 685		
RA	RESULT 2 Q9HGCV1 PRELIMINARY;		
RA	ID Q9HGCV1 AC Q9HGCV1;		
RA	DT 01-MAR-2001 (T-EMBLrel. 16, Created)		
RA	DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)		
RA	DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
RA	DE SUP35 aliasuppressor mutant sal3-4.		
RA	GN OS Saccharomyces cerevisiae (Baker's yeast).		

213	PKVEDLKISESTHTNNANVTSADALIKEQQEPPVDEDEVNDMFGKDHDVSLI.FMGHVDAG	272
220	-----DVKUNLKVKEPAPDPSOVSSESSD-----KFOFDVDRFEDVNDMEGKHDV-----T	275

RESULT 6
Q6FVM2
TD_GCFM2
DDFTM1MADY.
DDFTM1MADY.
DDFTM1MADY.

RESULT 6

Qy	273	KSTMCNNLILYLTSYDKRTRIEKYERAKDAGRCGYLSTVMDTNKEERNDGKTEVGKAY	332	1	MSDSNQGNNQNYQQYSONGNQOOGNNRQGY-QAYNAQAQPAGGYQNYQGY-SGQGG 59	
Db	276	KSTMCNNLILYLTSYDKRTRIEKYERAKDAGRCGYLSTVMDTNKEERNDGKTEVGKAY	335	1	MSDPNQ-NQG----Q-GGQQIAQGGNYQYYQYQKLTQAQ-AGGYQPYGGGY-GG 49	
Qy	333	FETEKRRTTIDAPGKHMVYSEMGASSQADGVYLIVISARKGEYETGFERGGOTREHAL	392	60	YQQYQDAGYQQQYNPOGGYQ-OYNPOGGYQQQFNPOGGRGNYKNFNYYNNLQCYQAGFQ 118	
Db	336	FETEKRRTTIDAPGKHMVYSEMGASSQADGVYLIVISARKGEYETGFERGGOTREHAL	395	50	YGGYQPYGGYQFY-QDQQQAQGGATGNYPYO-AQGAPGGN-NYNNQFQD----Q 98	
Qy	393	AKTQGYNNKVVVNNKDDPTVNSKERYOCVNSVNSNPFRAIGNIKTQTVFNPVSGYSG	452	119	POSQMSLNDFOQQ--KQAAKPKPKTLKVSSGKILANAKTKVKGKPAESDKKEBEK 175	
Db	396	AKTQGYNNKVVVNNKDDPTVNSOBERVQCVNSVNSNLYLKAIGNVVKQDVENVFVSGYSG	455	99	QQSQGMMTLDDFHKQKQTSQASAPPQQKSLKLVSSGKILANAK--KPKEDKEKEEP 154	
Qy	453	ANLKDHDVDPKBCPWTGPTTLEYLDTMHNVDRHINAPMLPIAKMKDGTIVEGKIESG	512	176	SAETK--EPTKPTKVEEPVKEKEPKVOTEKEETKSBDPKVDEKLKISFSTHTNTNANTV 233	
Db	456	AGLKRVRKREBCPWTGPALEYLDEMRKDHYNAPMLPIAKMKDGTIVEGKIESG	515	175	KKEKKAKEKEQESKKEE-KRGTPRPAADEKEDEPKLEKLKIE--EOAANAS 210	
Qy	513	HIIKGQSTLMPNKTAVELQNYINNETENYDMANCGEQYKLRIKGVEEDDISPGFVLTSP	572	Qy	234	SADALIKEKEQEEVYDDEYVNDMFGGKDKHVSLLFEMGHVDACKSTMCGNLLYLGTGSYDKRTE 293
Db	516	HIIKGQSTLMPNKTPEVQNYINNETENYDMANCGEQYKLRIKGVEEDDISPGFVLTSP	575	Db	211	GADSLIKEKEQEEVYDGVNDMFGRDHMSIIPMGHVDAGRSTMCGNLLYMTGSYDKRTE 270
Qy	573	KNPPIKSVTVAQIAIVEKLSIANGSCVMVHATAIEVHAYELLIKKEKGTRNKSXKP	632	Qy	294	KYEREAQDKAGRCGMYLISNYMDTNKEERDGKTEEVGKAYFETEKRYTILDAGCHKMYS 353
Db	576	KNPPIKSVTVAQIAIVEKLSIANGSCVMVHATAIEVHAYELLIKKEKGTRNKSXKP	635	Db	271	KYEREAQDKAGKGWYLSWYMDTNREERDGKTEEVGRAYFETEKRYTILDAGCHKMYS 330
Qy	633	PAFAKGMKVIAVLETAPEVPCVETYQDYGFLRDLQDTTIAIGKTVKIAE	685	Qy	354	EMIGGASQADGVGLVISAARKGEYETGFERGGOTREHALAKTQCVNKLIVTINKMDDPV 413
Db	636	PAFAKGMKVIAVLETAPEVPCVETYDYPOLGFLRDLQDTTIAIGKTVKIE	688	Db	331	EMIGGASQADGVGLVISAARKGEYETGFERGGOTREHALAKTQCVNKLIVTINKMDDPV 390
RESULT 7						
Q9HGT4		PRELIMINARY;	PRT;	662	AA.	
AC	Q9HGT4;					
DT	01-MAR-2001	(TREMBureL 16, Created)				
DT	01-TUN-2001	(TREMBureL 17, Last sequence update)				
DT	01-MAR-2004	(TREMBureL 26, Last annotation update)				
DE		Polypeptide release factor 3.				
GN		Name=sup25;				
OS		Zygosaccharomyces rouxii (Candida mogii).				
OC		Saccharomyces; Fungi; Ascomycota; Saccharomycetes;				
OC		Saccharomycetales; Saccharomyceae; Zygosaccharomyces.				
NCBI_TaxID	4956;					
RN		[1]				
RP		SEQUENCE FROM N.A.				
RX		MEDLINE=21324110; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3;				
RA		Nakayashiki T.; Ebihara K.; Bannai H.; Nakamura Y.;				
RT		"Yeast (PSI+)" 'prions' that are cross-transmissible and susceptible				
RT		beyond a species barrier through a quasi-prion state.";				
RL		EMBL; AB319753; BAB12684.2;				
DR	GO; GO:0005525;	GTp binding; IEA.				
DR	GO; GO:003747;	translation release factor activity; IEA.				
DR	GO; GO:0006412;	P:protein biosynthesis; IEA.				
DR	GO; GO:00015;	P:translational termination; IEA.				
DR	InterPro; IPR004160;	EFTU C-term.				
DR	InterPro; IPR004161;	EFTU D2.				
DR	InterPro; IPR009001;	Elong-init C.				
DR	InterPro; IPR009095;	Protsyn Grpbind.				
DR	InterPro; IPR009000;	Translat factor.				
DR	InterPro; IPR00985;	Yeast_ERF.				
PFam;	PF00009;	GTP_EFTU; 1.				
PFam;	PF03144;	GTP_EFTU D2; 1.				
DR	PF03143;	GTp_EFTU D3; 1.				
DR	PRINTS;	PRO3315; ELONGATNEFT.				
DR	PROSITE; PS03031;	EFACTOR_GTP; UNKNOWN_1.				
KW	GTp-binding; protein biosynthesis.					
SEQUENCE	662 AA;	73780 MW;	26110461.99FB1E04	CRC64;		
SEQUENCE	70.9%;	Score 2549.5;	DB 2;	Length 662;		
Best Local Similarity	74.0%;	Pred. No. 5.2e-122;				
Matches	512;	Conservative 53;	Mismatches 90;	Indels 37;	Gaps 15;	
RESULT 8						
Q6CQF8		PRELIMINARY;	PRT;	700	AA.	
ID	Q6CQF8;					
AC	Q6CQF8;					
DT	25-OCT-2004	(TREMBureL 28, Created)				
DT	25-OCT-2004	(TREMBureL 28, Last sequence update)				
DT	25-OCT-2004	(TREMBureL 28, Last annotation update)				
DE		Similarity.				
ORFnames		KLAA0D1714249;				
GN		Kluveromyces lactic NRRL Y-1140.				
OS		Eukaryota; Fungi; Ascomycota; Saccharomyces.				
OC		Saccharomyces; Saccharomyces cerevisiae; Kluyveromyces.				
NCBI_TaxID		NCBI TaxID=284590;				
OX		[1]				
RN		SEQUENCE FROM N.A.				
RP		STRAIN=NRRL Y-1140;				
RC						
RG		Genelvares;				
RA		Lafontaine I.; de Montigny J.; Marc C.; Neuveglise C.; Talia E.;				
RA		Goffard N.; Frangeul L.; Aigle M.; Anthouard G.; Bapour A.; Barbe V.,				
RA		Boirame S.; Blanchin S.; Becker J.M.; Beyne E.; Bleykasten C.,				
RA		Boirame A.; Boyer J.; Cattolico L.; Confioliolier F.; de Daruvar A.,				
RA		Desponts L.; Fabre E.; Fairhead C.; Ferry-Dumazet H.; Groppi A.,				

RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lescot I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennee D., Tekaya F., Wesołowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivianovic I., Bolotin-Fukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gailardin C., Weissenbach J., Winzer P., Souciet J.-L.	493 PIAAKWMDLGLTIVEGKIESGHKKGOSTLMPNKTAVEIQINQYNETENEYDMAMGGEQVK 552 RA 507 PIASKNQKDMGTVVEGIESGHIRKENQTLMPNTRSEVLIYTNTESYDMAVGEQVR 566
RA	"Genome evolution in yeasts."; RN [2]	553 LRIKGYVEEDLSPGFLTSKPNPIKVTKYEAQILIVELKSLIAAGFSCVMHHTAAIEV 612 RA 567 LRIKGYVEEEETSAQFVLTSPKPNPVQNTREVAQATIVELKSIMSGFSCVMHHTAAIEV 626
RA	SEQUENCE FROM N.A.	613 HIVLILHKLEGTKNSKSKPFAFKGMKVTAVLTEAPVCVETYDYPQLGRTFLRDQ 672
RA	SEQUENCE FROM N.RL Y-114;	627 TVTRLHKLEGTKNSKSKPFAFKGMKIAVIEVNEPVCVETDDYPQLGRTFLRDQ 686
RA	Genoscope; Submitted (JUL-2004) to the EMBL/GenBank/DDJB databases.	673 TTIAGKVKIAE 685
DR	EMBL; CR38124; CAH00927.1;	Db 687 TTIAGKVKVILE 699
DR	GO: 0005525; F: GTP binding; IEA.	Db 690 TTIAGKVKVILE 699
DR	GO: 0003747; F: translation release factor activity; IEA.	Db 691 TTIAGKVKVILE 699
DR	GO: 0006412; P: protein biosynthesis; IEA.	Db 692 TTIAGKVKVILE 699
DR	GO: 0006415; P: translational termination; IEA.	Db 693 TTIAGKVKVILE 699
DR	InterPro; IPR004160; EFTU C-term.	Db 694 TTIAGKVKVILE 699
DR	InterPro; IPR004161; EFTU D2.	Db 695 TTIAGKVKVILE 699
DR	InterPro; IPR004162; Elong init C.	Db 696 TTIAGKVKVILE 699
DR	InterPro; IPR005001; Protsyn_GTPbind.	Db 697 TTIAGKVKVILE 699
DR	InterPro; IPR005795; Yeast_ERF.	Db 698 TTIAGKVKVILE 699
Pfam	PF00009; GTP_EFTU; 1.	Db 699 TTIAGKVKVILE 699
Pfam	PF03144; GTP_EFTU_D2; 1.	Db 700 TTIAGKVKVILE 699
DR	Pfam; PF03143; GTP_EFTU_D3; 1.	Db 701 TTIAGKVKVILE 699
DR	PRINTS; PR00315; ELONGATNFTCT.	Db 702 TTIAGKVKVILE 699
DR	PRINTS; PR01343; YEASTERF.	Db 703 TTIAGKVKVILE 699
DR	PROSITE; PS00301; EFACTOR_GTP; UNKNOWN_1.	Db 704 TTIAGKVKVILE 699
KW	GTP-binding; Protein biosynthesis.	Db 705 TTIAGKVKVILE 699
SEQUENCE	700 AA; 77638 MW; 53F9905442F6B025 CRC64;	Db 706 TTIAGKVKVILE 699
Query Match	Score 2471; DB 2; Length 700;	Db 707 TTIAGKVKVILE 699
Best Local Similarity	68.8%; Pred. No. 5.6-118;	Db 708 TTIAGKVKVILE 699
Matches 500;	Conservative 56; Mismatches 95; Indels 82; Gaps 15;	Db 709 TTIAGKVKVILE 699
Qy	1 MSD-SNQGNNQ-QNYQYQSONGNOQQGNTRYQGYQAYNAQAQPGAGGYQNYQGSGYQGS 58	Db 710 TTIAGKVKVILE 699
Db	1 MSDQQRQDGQGQGQNQYQGNQYQGNQYQGYQSYNGQ-QGAQPGQYQAYAQGQPGQ 58	Db 711 TTIAGKVKVILE 699
Qy	59 GYQQYNPDAQYQQQTNPQGGYQQYNPQGGYQQFN-POGGRGNTYNTNN------NL 110	Db 712 TTIAGKVKVILE 699
Db	59 AYQGYNPQQA-QGIQP---YQGYNAQ---QGYNAQQGHNNNTNNKNTNNKSYNNYK 110	Db 713 TTIAGKVKVILE 699
Qy	111 QGYQ-----AGFOPOSQGMSLNFQKQQA-APKPKTTLKLVSSSGIKLA 155	Db 714 TTIAGKVKVILE 699
Db	111 QSYQAGQGYNQQPTGYAAPAQSSQSMTLKDQNQGSTMAAKRKPKLKLASSSGIKLV 170	Db 715 TTIAGKVKVILE 699
Qy	156 NATKRYGTKPKAESDKKEEKAETKEPTKEPTKEPTKEPTKESELPRV 215	Db 716 TTIAGKVKVILE 699
Db	171 GAKKPVAPK-----TEKIDESKEATK-----TTDNEEAQSELPKI 206	Db 717 TTIAGKVKVILE 699
Qy	216 EDLKISE-----STINTNNNNTSA-----DALIKEQEDEVDEVN 252	Db 718 TTIAGKVKVILE 699
Db	207 DDLK1SEAEPKTKTENTPSADDTSSEKTSKAKDTGGANSVDAIKEQDEVDEEVVK 266	Db 719 TTIAGKVKVILE 699
Qy	253 DMFGGKDHVSLIFMGHVDAGKSTMGGNLYLTSYDKRTEKYEAKDAGRCGMYLSSV 312	Db 720 TTIAGKVKVILE 699
Db	267 DMFGGKDHVSLIFMGHVDAGKSTMGGNLYLTSYDKRTEKYEAKDAGRCGMYLSSV 326	Db 721 TTIAGKVKVILE 699
Qy	313 MDTNKEBRNDKTIIEKGKAYPTEKECRYTILDAPGKHMVYSEMIGQASDVGVLVTSR 372	Db 722 TTIAGKVKVILE 699
Db	327 MDTNKEBRNDKTIIEKGKAYPTEKECRYTILDAPGKHMVYSEMIGQASDVGVLVTSR 386	Db 723 TTIAGKVKVILE 699
Qy	373 KGEYETGPERGQTRBHALAKTQGYNNVQDNKTYCQVSVNSFLR 432	Db 724 TTIAGKVKVILE 699
Db	387 KGEYETGPERGQTRBHALAKTQGYNNVQDNKTYCQVSVNSFLR 446	Db 725 TTIAGKVKVILE 699
Qy	433 AIGYNKTDYMPVSSYSGANLKDHPKCPWYTGPTLLEYDLMNHYDRHINAPFL 492	Db 726 TTIAGKVKVILE 699
Db	447 AVGYNVREDVIFMPVSEYTAGLKERDVKPCWPTGSPSLUEYDLMNKTDRHINAPFL 506	Db 727 TTIAGKVKVILE 699
Qy	450 1 MSD-SNQGNNQ-ONTQYSQNGNQOGNNQYQGYQAYNAQAQPGAGGYQNYQGSGYQGS 58	Db 728 TTIAGKVKVILE 699
Db	1 MSDQQRQDGQGQNQYQGNQYQGYQSYNGQ-QGAQPGQYQAYAQGQPGQ 58	Db 729 TTIAGKVKVILE 699
Qy	59 GYQQYNPDAQYQQQTNPQGGYQQYNPQGGYQQFN-POGGRGNTYNTNNKNTNNKSYNNYK 110	Db 730 TTIAGKVKVILE 699
Db	59 AYQGYNPQQA-QGYQP---YQGYNAQ---QGYNAQQGHNNNTNNKNTNNKSYNNYK 110	Db 731 TTIAGKVKVILE 699
Qy	111 QGYQ-----AGFOPOSQGMSLNFQKQQA-APKPKTTLKLVSSSGIKLA 155	Db 732 TTIAGKVKVILE 699
Db	111 QSYQAGQGYNQQPTGYAAPAQSSQSMTLKDQNQGSTMAAKRKPKLKLASSSGIKLV 170	Db 733 TTIAGKVKVILE 699
Qy	156 NATKRYGTKPKAESDKKEEKAETKEPTKEPTKEPTKESELPRV 215	Db 734 TTIAGKVKVILE 699
Db	171 GAKKPVAPK-----TEKIDESKEATK-----TTDNEEAQSELPKI 206	Db 735 TTIAGKVKVILE 699
Qy	216 EDLKISE-----STINTNNNNTSA-----DALIKEQEDEVDEVN 252	Db 736 TTIAGKVKVILE 699
Db	207 DDLK1SEAEPKTKTENTPSADDTSSEKTSKAKDTGGANSVDAIKEQDEVDEEVVK 266	Db 737 TTIAGKVKVILE 699
Qy	253 DMFGGKDHVSLIFMGHVDAGKSTMGGNLYLTSYDKRTEKYEAKDAGRCGMYLSSV 312	Db 738 TTIAGKVKVILE 699
Db	267 DMFGGKDHVSLIFMGHVDAGKSTMGGNLYLTSYDKRTEKYEAKDAGRCGMYLSSV 326	Db 739 TTIAGKVKVILE 699
Qy	313 MDTNKEBRNDKTIIEKGKAYPTEKECRYTILDAPGKHMVYSEMIGQASDVGVLVTSR 372	Db 740 TTIAGKVKVILE 699
Db	327 MDTNKEBRNDKTIIEKGKAYPTEKECRYTILDAPGKHMVYSEMIGQASDVGVLVTSR 386	Db 741 TTIAGKVKVILE 699
Qy	373 KGEYETGPERGQTRBHALAKTQGYNNVQDNKTYCQVSVNSFLR 432	Db 742 TTIAGKVKVILE 699
Db	387 KGEYETGPERGQTRBHALAKTQGYNNVQDNKTYCQVSVNSFLR 446	Db 743 TTIAGKVKVILE 699
Qy	433 AIGYNKTDYMPVSSYSGANLKDHPKCPWYTGPTLLEYDLMNHYDRHINAPFL 492	Db 744 TTIAGKVKVILE 699
Db	447 AVGYNVREDVIFMPVSEYTAGLKERDVKPCWPTGSPSLUEYDLMNKTDRHINAPFL 506	Db 745 TTIAGKVKVILE 699

QY	156	NATKKVGTPKPAESDKKEBKSAAETKEPTKEPTKVEEPVKQVOTEKEEEKVTEEKTEKEPKV	215	DR	Pfan; PR03144; GTP EFTU D2; 1.
QDB	171	GACKPVAPK-----TKEKTDSEKAATK-----TTDNEEAQSELPEKTI	206	DR	PRINTS; PR0315; BIOLGATINFCFT.
QY	216	EDLKISE-----SHTNINNANTSA-----DALIREEEYDDEVN	252	DR	PRINTS; PR0143; YEASTER.F.
QDB	207	DDLKISEAKPKTKENTPADDISSEKTSAKADTSTGGANSVDALIKEQDEVDEEVK	266	DR	PROSITE; PS0301; EFACTOR GTP; UNKNOWNN_1.
QY	253	DMFGGKDHTSLIEMGHVDAKGSTMGNLILYLTGSVDRKTIYEKREAKDAGRCWYLSW	312	KW	GTP-binding; Protein biosynthesis.
QDB	253	DMFGGKDHTSLIEMGHVDAKGSTMGNLILYLTGSVDRKTIYEKREAKDAGRCWYLSW	312	SEQUENCE	691 AA; 76193 MW; 833803C60B9509 CRC64;
QY	267	DMFGGKDHTSLIEMGHVDAKGSTMGNLILYLTGSVDRKTIYEKREAKDAGRCWYLSW	326	Query Match	68 6%; Score 2464; DB 2; Length 691;
QDB	313	MDTNKEERNDGKTEIEVGKAYFETEKRTYRILDAFGHKNMVSMEIGGASADVGVIVSAR	372	Best Local Similarity	71.1%; Pred. No. 1.3e-117;
QY	3227	MDTNKEERNDGKTEIEVGKAYFETEKRTYRILDAFGHKNMVSMEIGGASADVGVIVSAR	386	Matches	52; Mis matches 93; Indels 58; Gaps 17;
QDB	373	KGBETGFRERGQPREHALLAKTQGVNRMVWVNNRMDDTVAKSERTDQCVSNSNFR	432	QY	5 NOGRNQNTQOQYSONGNOQGNNYQY--QANNAQOQAGGY--YQHNFQ--GYSQY 55
QY	3887	KGEYETGFEGKGQTREHALLAKTQGVNRMVWVNNRMDDTVAKSERTDQCVSNSNFR	446	Db	25 NQGQQNQGQYNNPSNFQ--NYQGYVPOGGCQAYQGQAGGYQYANQOQAGGYQY 80
QDB	4333	AINYNKTDVVFMPVSGYSGANLKDHDPRECPNPTGPTILLEYDLDTNHNDRHNAPML	492	QY	56 QQQGQQQNP-DAGYQQQYNPQGGYQYQONPQGGYQ--QOFN--PQGGRGNYKPNFYNNNL 110
QY	447	AVGNVKEEYD1FMPVSGYTAGLKERDVKDPCWYTGPLLEYDLMKCTDRHNAPML	506	Db	81 Q--GQQTNPQAQGQ--GQQTNPQAQGQ--GQQTNPQAQGQ--GQQTNPQAQGQ-- 128
QDB	493	PIAAKMDQDTIVEGKIEGHIKKGQSTILMPNKTAVELONIYNETENEDVAMCGEQVK	552	QY	111 QGYQAGFQPOSGQNSLNDFOK--QQKOAAPKPKTCLKVSSG1KLNATKVKGTGPKAES 168
QY	507	PIASMKMDQDTIVEGKIEGHIKKGQNTLMPNRTSVEILTYNETESVDMAVCGEQVK	566	Db	129 QG--OSATAPVILNNFEKGTVPNATAPKPKTCLKASSG1KLNATKVKGTGPKVA----- 177
QDB	553	LRIKGVVEEDISPGFVPLTSKPNPKTISVTRFAVQIAVEILS1AAGFSVCMVHTAIEV	612	QY	169 DKKEEKAETKEPKTKEPKT--VTEPVKEEKPQTCRTEKEPKTKEPKTKEPKTKEPKT-- 223
QY	567	LRIKGVVEEISAGFVPLTSKPNPKTAVTIEAFCVTEQYDQYFQLGRFTLROG	626	Db	178 -KKEE--AKAEPEPKKEPKSSAEGPKSEDATASEDRA-----VPSIEKL1SEADTA 228
QDB	6113	HIVKLHKLEKGTMNRSKPAPAFARKGMKVIATLEAPCVCTYQDYFQLGRFTLROG	672	QY	224 -THINTNNANNTSADALIKEQEEVDEVNDFMGKDHVSLIMFQHVDACKSTMGNNLY 282
QY	6227	TVTRLLHKLEKGGSNRSKPAPAFARKGMKVIATLEAPCVCTYQDYFQLGRFTLROG	686	Db	229 KKDADAAATGATSSDALLIKEQEDETVEVVKDFMGKDHVSLIMFQHVDACKSTMGNNLY 288
QDB	673	TTIAIGKIKIAE 685	700	QY	283 LTGSYDKEKTRTEKYEAKDAGRCWYLSWMDTNRKBERNDGKTELVGKAYFETECKRTYI 342
QY	687	TTIAIGKIKIAE 699	700	Db	289 LTGSYDKEKTRTEKYEAKDAGRCWYLSWMDTNRKBERNDGKTELVGKAYFETECKRTYI 348
QDB	RESULTS 10			QY	343 LDAPGHRMYSSEMIGGASQADGVVILVISARKGEETGFERGGQPREHALLAKTQGVNKNV 402
QY	Q750T4	PRELIMINARY;	PRT;	Db	349 LDAPGHRMYSSEMIGGASQADGVVILVISARKGEETGFERGGQPREHALLAKTQGVNKNV 408
QDB	Q750T4	PRELIMINARY;	PRT;	QY	403 VVNNRMDDP7PVNWSKERYDOCVSNVSNPFLRAIGTNKTDVVFMPVSGYSGANLKHVDPK 462
QY	0750T4	PRELIMINARY;	PRT;	Db	409 VVNNRMDDP7PVNWSKERYDOCVSNVSNPFLRAIGTNKTDVVFMPVSGYSGANLKHVDPK 468
QDB	0750T4	PRELIMINARY;	PRT;	QY	463 ECPNTGPTPLEYDPMHVDRHNAPMFLPIAKMDQDTIVEGKIEGHIKKGQSTLL 522
QY	05-JUL-2004	(TREMBrel. 27, Created)		Db	469 DCPWYDGPSSLEYDPMHVDRHNAPMFLPIAKMDQDTIVEGKIEGHIKKGQSTLL 528
QDB	05-JUL-2004	(TREMBrel. 27, Last sequence update)		QY	523 MPNKTAVELONIYNETENEDMAGEQVKLRIKVEEEDISPGVLTSPSKNPKTISVTKF 582
QY	AGL145WP	(TREMBrel. 27, Last annotation update)		Db	529 MPNKPVEILIAQNETEQVDMAVGQEVRLRIGVEEEEDISAGGVLTSPSKNPKTISVTKF 588
QDB	ORNNames-AGL145WP			QY	583 VAQIAI1VELKSIIAAGFSCMVHWTIAEEHV1VLLHKLEKGTMNRSKPAPAFARKGMKV 642
QY	NCBI_TaxID-33169;			Db	589 VDQI1A1VELKSIIAAGFSCMVHWTIAEEHV1VLLHKLEKGTMNRSKPAPAFARKGMKV 648
QDB	SEQUENCE FROM N.A.			QY	643 IAVLIEAPEPVCVETYDYPOLGRFTLRDGQTIAIGKIVKIAE 685
QY	STRAIN=ATCC 10895;			Db	649 IAVLIEAPEPVCVETYDYPOLGRFTLRDGQTIAIGKIVKILE 691
QDB	Lerch A., Brachat S., Voegeli S.E., Gaffney T., Philippson P.,			RESULT 11	
QY	RA			Q9HG17	
QDB	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.			AC	
QY	EMBL; A0516820; AA554346.1;			ID	
QDB	AGD; AGL145W; -;			Q9HG17;	
QY	GO; GO:0005525; P:GTP binding; IEA.			DT	
QDB	GO; GO:0003747; P:translation release factor activity; IEA.			01-NAR-2001 (TREMBrel. 16, Created)	
QY	GO; GO:0006412; P:protein biosynthesis; IEA.			01-JUN-2001 (TREMBrel. 17, Last sequence update)	
QDB	GO; GO:0006415; P:translational termination; IEA.			01-NAR-2004 (TREMBrel. 26, Last annotation update)	
QY	InterPro; IPR004161; EPrU D2.			DE	
QDB	InterPro; IPR009001; Elong Init C.			Name-sup5;	
QY	InterPro; IPR00793; ProtSyn GrPbind.			GN	
QDB	InterPro; IPR009000; TranslC factor.			OS	
QY	InterPro; IPR00225; yeast-ERF.			OC	
QDB	InterPro; IPR00092; GTP EFTU.			OC	
QY	InterPro; IPR000793; Saccomycota; Saccharomyces; Saccharomyces;			NCB1 TaxID:5419;	
QDB	Eukaryota; Fungi; Ascomycota; Saccharomyces; Candida.			NCB1 TaxID:1449;	

DR	EMBL; AY553984; AAS64325.1;	DR	EMBL; AY553988; AAS64329.1;
DR	GO; GO:000525; F:GTP binding; IEA.	DR	GO; GO:000525; F:GTP binding; IEA.
DR	GO; GO:003747; F:translational release factor activity; IEA.	DR	GO; GO:0003747; F:translational release factor activity; IEA.
DR	GO; GO:006412; P:protein biosynthesis; IEA.	DR	GO; GO:006412; P:protein biosynthesis; IEA.
DR	GO; GO:006415; P:translational termination; IEA.	DR	GO; GO:006415; P:translational termination; IEA.
DR	InterPro; IPR00795; ProSyn GTPbind.	DR	InterPro; IPR00795; ProSyn GTPbind.
DR	InterPro; IPR003285; Yeast ERF.	DR	InterPro; IPR003285; Yeast ERF.
PRINTS	PR00315; BLONGATNFCFT.	PRINTS	PR00315; BLONGATNFCFT.
PRINTS	PR01343; YEASTERF.	PRINTS	PR01343; YEASTERF.
DR	PROSITE; PS00301; EFACTOR_GTP; UNKNOWN_1.	DR	PROSITE; PS00301; EFACTOR_GTP; UNKNOWN_1.
KW	GTP-binding; Protein biosynthesis.	KW	GTP-binding; Protein biosynthesis.
FT	NON_TER 1	FT	NON_TER 1
FT	NON_TER 435 435 AA; 49026 MW; EDCD79569A7FF9892 CRC64;	FT	NON_TER 435 435 AA; 49081 MW; 39A0CA0A01F8D8EB CRC64;
SQ	SEQUENCE 435 AA;	SQ	SEQUENCE 435 AA;
Query Match Score 63.9%; Best Local Similarity 99.8%; Matches 434;保守性 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 63.6%; Best Local Similarity 99.3%; Matches 432;保守性 1; Mismatches 2; Indels 0; Gaps 0;		
Qy	8 NNQNYQQYSQSONQOQNNRYYQGQAYNAQAAQPGAGYYQNYQGSGYQQGYYQYNPDA	Qy	8 NNQNYQQYSQSONQOQNNRYYQGQAYNAQAAQPGAGYYQNYQGSGYQQGYYQYNPDA
Db	1 NNQNYQQYSQSONQOQNNRYYQGQAYNAQAAQPGAGYYQNYQGSGYQQGYYQYNPDA	Db	1 NNQNYQQYSQSONQOQNNRYYQGQAYNAQAAQPGAGYYQNYQGSGYQQGYYQYNPDA
Qy	68 GYQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGG	Qy	68 GYQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGG
Db	61 GYQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGG	Db	61 GYQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGGQQINPQGG
Qy	128 DFOKQOKOAAAPRKPKTTLKLVSSGGIKLANATKVKVGTKPARESDKKEPEKSARTKEPTKEPT	Qy	128 DFOKQOKOAAAPRKPKTTLKLVSSGGIKLANATKVKVGTKPARESDKKEPEKSARTKEPTKEPT
Db	121 DFOKQOKOAAAPRKPKTTLKLVSSGGIKLANATKVKVGTKPARESDKKEPEKSARTKEPTKEPT	Db	121 DFOKQOKOAAAPRKPKTTLKLVSSGGIKLANATKVKVGTKPARESDKKEPEKSARTKEPTKEPT
Qy	188 KVEEPYKKEKEPKVQTEBKTKEKSLEPKVEDLKSISESTHTNNNTNTSADALIKEQEEVD	Qy	188 KVEEPYKKEKEPKVQTEBKTKEKSLEPKVEDLKSISESTHTNNNTNTSADALIKEQEEVD
Db	181 KVEEPYKKEKEPKVQTEBKTKEKSLEPKVEDLKSISESTHTNNNTNTSADALIKEQEEVD	Db	181 KVEEPYKKEKEPKVQTEBKTKEKSLEPKVEDLKSISESTHTNNNTNTSADALIKEQEEVD
Qy	248 DEVNDMFGGDKDHVSLJFMGVDAKGSTMCGNLLYTGSVKRTEKVKYERAKDAGRQW	Qy	248 DEVNDMFGGDKDHVSLJFMGVDAKGSTMCGNLLYTGSVKRTEKVKYERAKDAGRQW
Db	241 DEVNDMFGGDKDHVSLJFMGVDAKGSTMCGNLLYTGSVKRTEKVKYERAKDAGRQW	Db	241 DEVNDMFGGDKDHVSLJFMGVDAKGSTMCGNLLYTGSVKRTEKVKYERAKDAGRQW
Qy	308 YLSWMNDTNKBERNDGKTIKEVKAYPETEKRYTILDAPGHKMYVSEMGGAQADVGVL	Qy	308 YLSWMNDTNKBERNDGKTIKEVKAYPETEKRYTILDAPGHKMYVSEMGGAQADVGVL
Db	301 YLSWMNDTNKBERNDGKTIKEVKAYPETEKRYTILDAPGHKMYVSEMGGAQADVGVL	Db	301 YLSWMNDTNKBERNDGKTIKEVKAYPETEKRYTILDAPGHKMYVSEMGGAQADVGVL
Qy	368 VISARKGEYETGPERGGOTREHALLAKTQGVMKVVVVKMDDPTVNSKERYDQCVSNV	Qy	368 VISARKGEYETGPERGGOTREHALLAKTQGVMKVVVVKMDDPTVNSKERYDQCVSNV
Db	361 VISARKGEYETGPERGGOTREHALLAKTQGVMKVVVVKMDDPTVNSKERYDQCVSNV	Db	361 VISARKGEYETGPERGGOTREHALLAKTQGVMKVVVVKMDDPTVNSKERYDQCVSNV
Qy	428 SNFLRAGYNIKTDV 442	Qy	428 SNFLRAGYNIKTDV 442
Db	421 SNFLRAGYNIKTDV 435	Db	421 SNFLRAGYNIKTDV 435

Search completed: July 1, 2005, 18:19:51
Job time : 113.109 secs
RESULT 15
Q6Q712

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database :									
1: geneseqp1980s:*	A_Geneseq_16Dec04:*								
2: geneseqp1980s:*									
3: geneseqp2000s:*									
4: geneseqp2001s:*									
5: geneseqp2002s:*									
6: geneseqp2003as:*									
7: geneseqp2003bs:*									
8: geneseqp2004s:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	3594	100.0	685	4	AAB30792	Amino acid	PF	09-JUN-2000; 20000WO-US015876.	XX
2	3594	100.0	685	6	ABR53107	Protein S	PR	09-JUN-1999; 99US-0138833P.	XX
3	3594	100.0	685	7	ADK63022	Disease t	(ARCH-)	ARCH DEV CORP.	XX
4	2345	65.3	721	5	ABP73437	Candida a	PI	Lindquist S, Li L, Ma J, Liu J, Sondheimer N, Scheibel T;	XX
5	2177	60.6	715	4	AAB30820	Amino acid	DR	WPI; 2001-061723/07.	XX
6	1679	46.7	741	4	AAB30819	Amino acid	DR	N-PSDB; AAC86769.	XX
7	1658	46.1	690	8	ADS44300	Bacteri	PD	14-DEC-2000.	XX
8	1557	43.3	720	7	ADB70240	C. neoform	PD	WO200075324-A2.	XX
9	1557	43.3	716	6	ABJ26505	Aspergill	XX		
10	1519	42.3	712	6	ABJ25450	Aspergill	PT	New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers.	XX
11	1364	38.0	634	7	ADM04489		PT	Claim 11; Page 125-127; 18pp; English.	XX
12	1354	35.5	37.7	499	7	ADC35080			
13	1354	35.5	37.7	499	8	ADN03793			
14	1354	35.5	37.7	499	8	ADP54304			
15	1354	35.5	37.7	499	8	ADP47765			
16	1354	35.5	37.7	499	8	ADR99225			
17	1346	35.5	37.5	628	8	ADN99777			
18	1345	35.5	37.4	628	4	AAB7825			
19	1329	37.0	271	4	AAB30800	A modif			
20	1316	35.5	36.6	619	4	ABP62309			
21	1307	35.5	36.4	499	2	AABW7508			
22	1307	35.5	36.4	499	6	ABR07508			
23	1307	35.5	36.4	499	8	ADQ76523			
24	1260	35.1	504	4	AAB94470				
25	1097	30.5	215	4	AAB30799	A modif			

CC multiple reactivities, e.g. derivatised with enzymes, or specific binding
 CC partners, and useful e.g. for performing multi-step chemical reactions.
 CC They can be used to create an inducible, or stable phenotypic alteration in
 CC a cell, e.g. for gene therapy, protein production, imparting disease
 CC resistance to plants, altering plant pigmentation and for diagnosis and
 CC treatment of plant diseases

XX

Saccharomyces cerevisiae.
 OS
 XX
 EP1258494-A1.

XX

20-NOV-2002.

XX

20-DEC-2001; 2001EP-00130253.

XX

PR 15-MAY-2001; 2001EP-00111774.

XX

(CELL-) CELIZOME AG.

XX

Qy 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Db 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Qy 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Db 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Qy 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Db 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Qy 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Db 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Qy 241 EQEEVYDDEVNDMFGKDHVSLLFMGHYDAGKSTMGGNLLYLTGSVDRKTIKERYEAK 300
 Db 241 EQEEVYDDEVNDMFGKDHVSLLFMGHYDAGKSTMGGNLLYLTGSVDRKTIKERYEAK 300
 Qy 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Db 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Qy 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420
 Db 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420
 Qy 421 DQCVSNVSNFLRAIGYNTKIDVMPVSGSYGSGANLKDHYDPKCBPWTQPTLLEYDTMN 480
 Db 422 DQCVSNVSNFLRAIGYNTKIDVMPVSGSYGSGANLKDHYDPKCBPWTQPTLLEYDTMN 480
 Qy 481 HVDRHINAPPMPLIAAKMDLGTIVEGKLESGHIKKGQSTLMLNKTAEVIONYNETEN 540
 Db 481 HVDRHINAPPMPLIAAKMDLGTIVEGKLESGHIKKGQSTLMLNKTAEVIONYNETEN 540
 Qy 541 EVDMAMCGEYVKLRLKGVEBEDISGFVTSKPNPIKSTVTKVAQIAVBLKSLIAAGS 600
 Db 541 EVDMAMCGEYVKLRLKGVEBEDISGFVTSKPNPIKSTVTKVAQIAVBLKSLIAAGS 600
 Qy 601 CVMVHTA1BEVHTVYLHLKLEGTGTRNRSKSKPAPAKKMKVIAVLETAPVCVETYQY 660
 Db 601 CVMVHTA1BEVHTVYLHLKLEGTGTRNRSKSKPAPAKKMKVIAVLETAPVCVETYQY 660
 Qy 661 PQLGRFTLIRDQGTTIAIGKIVKIAE 685
 Db 661 PQLGRFTLIRDQGTTIAIGKIVKIAE 685

RESULT 2
 ABR33107
 1D ABR33107 standard; protein; 685 AA.
 XX
 AC ABR33107;
 DT 20-JUN-2003 (first entry)
 XX Protein sequence #SEQ ID 1079.
 DE XX
 KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX

Sequence 685 AA;

Query Match 100.0%; Score 3594; DB 4; Length 685;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 685; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; PT
 PA
 XX

Qy 1 Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 Db 1 Matzioch M, Schultz JD, Superi-Furga GB;
 Qy 61 WPI; 2003-250078/25.
 Db 61 DR N-PSDB; ACC61149.

XX
 New isolated protein complexes useful for diagnosing a disease or
 disorder, or as a target for an active agent of a pharmaceutical,
 preferably a drug target in the treatment or prevention of disease or
 disorder.

XX
 Disclosure; SEQ ID NO 1079; 17pp + Sequence Listing; English.

CC
 The invention relates to multiprotein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR568-ABR3903 and ABR601-AC61144 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this
 CC patent is not represented in the printed specification, but is based on
 CC sequence information supplied by the European Patent Office. The complete
 CC document is available on CD-ROM

XX
 SQ Sequence 685 AA;

Query Match 100.0%; Score 3594; DB 6; Length 685;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 685; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Db 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Qy 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Db 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Qy 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Db 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Qy 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Db 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Qy 241 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 240
 Db 241 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 240

Qy 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Db 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Qy 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420
 Db 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420
 Qy 421 DQCVSNVSNFLRAIGYNTKIDVMPVSGSYGSGANLKDHYDPKCBPWTQPTLLEYDTMN 480
 Db 422 DQCVSNVSNFLRAIGYNTKIDVMPVSGSYGSGANLKDHYDPKCBPWTQPTLLEYDTMN 480
 Qy 481 HVDRHINAPPMPLIAAKMDLGTIVEGKLESGHIKKGQSTLMLNKTAEVIONYNETEN 540
 Db 481 HVDRHINAPPMPLIAAKMDLGTIVEGKLESGHIKKGQSTLMLNKTAEVIONYNETEN 540
 Qy 541 EVDMAMCGEYVKLRLKGVEBEDISGFVTSKPNPIKSTVTKVAQIAVBLKSLIAAGS 600
 Db 541 EVDMAMCGEYVKLRLKGVEBEDISGFVTSKPNPIKSTVTKVAQIAVBLKSLIAAGS 600
 Qy 601 CVMVHTA1BEVHTVYLHLKLEGTGTRNRSKSKPAPAKKMKVIAVLETAPVCVETYQY 660
 Db 601 CVMVHTA1BEVHTVYLHLKLEGTGTRNRSKSKPAPAKKMKVIAVLETAPVCVETYQY 660
 Qy 661 PQLGRFTLIRDQGTTIAIGKIVKIAE 685
 Db 661 PQLGRFTLIRDQGTTIAIGKIVKIAE 685

Qy 100.0%; Score 3594; DB 6; Length 685;
 Best Local Similarity 100.0%; Pred. No. 2.9e-21;
 Matches 685; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Db 1 MSDSNQNNQNYOQOYOSQNGNQOQNNRQYQYNAQOQAGGYQNYQGSSYQQGY 60
 Qy 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Db 61 QQXNPDAIGTQQYQNNPQGGTQOYNPQGGTYQDQGNYKFNQNNNQGQAOFGPQ 120
 Qy 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Db 121 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 180
 Qy 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Db 181 EPTKEPTKVEBPVKKEKVKQTEETEKKSELPEKVEDLKISESTPHNTNANNTSADALIK 240
 Qy 241 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 240
 Db 241 SQGMSLNDFOQKQOAAAPPKKTLKLVSSSGIKLANATKVGKTPAEEKKBEKSAETK 240
 Qy 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Db 301 DAGRGWYLSWMDTNKEERNDGKTIKERYEAKFETEKRTYTLDAFGHMYVSEMGAS 360
 Qy 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420
 Db 361 QADYCVLVIISARKGEYETGPERGGOTREALLAKTQGVNRMVVVNRMDPTVNSKERY 420

The specification describes chimeric polypeptides which comprise at least one SCHAC (self-coalesces into higher order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases. The present sequence is used in the course of the invention

Sequence 715 AA:						
Query	Match	Score	DB 4;	Length	715;	
3Q	Best Local Similarity	65.3%;	2345.5;			
	Matches 471;	64.6%;	Pred. No. 2.2e-154;			
	Conservative	77;	Minmatches 120;	Indels 61;	Gaps 17;	
Dy	1	MSDSDQGNQNNQNYQQYQSONGHOQGNNRYQQYQAAQAAQ	-- -PAGGY - YQNYQGYSQ	54		
	2	MANASLNGDQSQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	-- -YNNPNAAOQSFVQQGTYQQQQQQQQQQQQQQQQQQQQ	53		
Dy	55	YQQ-GGTYQQYNP- DAGYQQTNPQQGYQQ-	-YNNPQQGYQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	111		
	54	QQYQGGNQNYQQGYQNTNNRGGYQQGYQNTNNRGGYQNTNN	-- -NRGGYQGYNQNGQYQG	110		
Dy	112	GYQA -GFQP----- -QSGQMSLNDFQKQ - -OKQAA - -	-PKPKKTLLKLVSSSGIKLAKNATK	159		
	111	GQQQYNSOPQQQQQQQQGMSLADFQKQTBEQASLINKPAVKTLKLAGSGIKLAKNATK	-- -PKPKTKEEPVK	170		
Dy	160	KVGT -KP-----	-AESDKEKEEKSATKEP	194		
	171	KVDTTSQPKSESSPAPAPAASASASAPQEEKEKEAAATPAAAAPETKEETSA	-PAETK	230		

The specification describes chimeric polypeptides which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatized with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used to create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases. The present sequence is used in the course of the invention

Seq	Sequence / ₁ AA:	Query Match	60.6%	Score	2177;	DB	4;	Length	741;
	Best Local Similarity	60.9%				Pred.	No. 1.2e-12;		
	Matches 433;	Conservative	87;	Mismatches	127;	Indels	64;	Gaps	15
Qy	11	QNYQQTSQNGNQQGNNTRYQQOAYNQAQPAGGYQNYQGYSYQQGXYQQINPDAQYQ	70						
Db	56	QQEQQFQQGQQQQTNQ-GGTNNYNNR--GGYNNRGYYNNNRGGYSNTN--SYN	107						
Qy	71	QQYNPQGGYQQYNPQGGYQQQFNPOGGGRGNYKNFNYNNN--LOGYQAFG----QPOSQ	122						
Qy	88								
Db	108	TNSN-QGGYSNTN-----	151						
Db	123	G-----MSLNDFOKQKQAA-----PKPKTTLKL-VSSSGIKLANKATKCVGTKPAB	168						
Qy	152	DQQQETSGQMSLEDYQKQRESLNKLTQKKVKLKNLNSSTYKAPIYTKKEEPEVHQ	211						
Qy	169	DKKEEERSAE---TKPEPKTKEPKVEE-----PVKKEEERPVQEPEBKTKEKS--EL	212						

Db	212 ESKTEBPAKEBEEKIQNEPAEAENKVEEESKVEAATPKVSESEFPAST- PTKTEAKASKEV 270	PT New recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
Qy	213 PKVEDLKKISESTHTNNNAAATNTSADALIKQEEFFVDEVVNDMFGKDKHVSLSIFMGHVTAG 272	PT
Db	271 AAAAALKEVSQAKKESSNTADLVKEEQEQQIDASINTDMFGKDKHVSLSIFMGHVTAG 330	PT
Qy	273 KSTMGGNLLYLTGSYDKTEKYEAKAGRCQWYLSKMTDNKEERNDGKTEVKGKAY 332	PT
Db	331 KSTMGGNLJPLTGAVDKTEKYEAKAGRCQWYLSKMTDNKEERNDGKTEVKGKAY 390	XX
Qy	333 FETEKRRYTLIDAPSHKMTVSEMMIGGASQADGVTLVIAARKGEYETGFRGGTREHAL 392	XX
Db	391 FETDKRRYTLIDAPSHKMTVSEMMIGGASQADGVTLVIAARKGEYETGFRGGTREHAL 450	XX
Qy	393 AKTQVYKMKVYVNNKMDPPTVNSKERYDOCVSVNYSVNFRLAIGYKNUVFMVSGYSG 452	XX
Db	451 AKTQVQVNLKVVNVNMDPPTVNSKERYBCTTKLAMYIKGVGQ-Q-KGQVLFMVSQGTTG 509	XX
Qy	453 ANLDHVDPKCECPWYTGPTLLEYLDTMHNHYDRHMAPNMLPIAAKMKDQGTVTEKGKSG 512	XX
Db	510 AGJLKEVSKDQDAPYNGPSLVEYDSDMLPLAVERKINDPMLPISSKMKDQGTVTEKGKSG 569	XX
Qy	513 HIKKQGSTLJLMPNTPAVEIQNTYETENEDTMAMCQEYQVTLRIGVEEDISPGFVLTSP 572	XX
Db	570 HVKKGQNLWLPNKTQVETTIVNTEAADSAPCGEQVRLRIGIEEDLSSAGYVLSI 629	XX
Qy	573 KNPPIKSVTKEVQAIAVELVLSKTTAAGFSCYMHVHTAIETVHVYVHLKLEKGUNRKSKP 632	XX
Db	630 NHPVKTVTRIAQIAVERVLSKTSILSTGFSVSCYMHVHTAIETVFTFOUHNHQKGTNRRSKA 689	XX
Qy	633 PAPAKKGMYIAVLETEAPCVCYETQDYLQGLGFTLROGTTIAIGTKVKT 683	XX
Db	690 PAPAKQGMKIAVLETTETPYCIESSYYDYLQGLGFTLROGTTIAIGTKVKT 740	XX
Qy	RESCUL 7	
Db	ADS44300 standard; protein: 690 AA.	
Qy	ADS44300	
XX	02-DEC-2004 (first entry)	
XX	Bacterial polypeptide #22730.	
XX	Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.	
OS		
XX	US2003233675-A1.	
XX	18-DEC-2003.	
XX	20-FEB-2003; 2003US-00369493.	
XX	21-FEB-2002; 2002US-0360039P.	
XX	(CROY/ CAO Y.	
PA	(HINKLE G. J.	
PR	(SLAT/ SLATER S. C.	
PA	(CHEN/ CHEN X.	
PA	(GOLD/ GOLDMAN B. S.	
XX	WPI; 2004-061375/06.	
Qy	CAO Y., Hinkle G.J., Slater SC, Chen X., Goldman BS;	
Db	520 TLJMKNTKAVEIQNTYETENEDTMAMCQEYQVTLRIGVEEDISPGFVLTSPKQPKIVS 579	
Qy	527 VLYMENQFLVETAYDAEDEEISSCQDVRURVRG-DDSDVQTGIVLTSTKAPVHAT 585	

Qy 580 TKEVQIAIVELKSLIAAGFSCMVHATAEEHVILKHLKEGTNTRSKKPPAFAKKG 639
 Db 586 TRPIAQIAILELPSLTTGYSVCMHATAEEVSAFKLHLKLDK-TNRSKKPPAFATKG 644

Qy 640 MKVIAVLETEAPVCVCTYQDFQLGRTLDRDQGTTIAKGKVKIAE 685
 Db 645 MKIAELEDTQFVCMERFEDYQYMGRTLDRDQGTTAVGKVKVILD 690

RESULT 8
 ADB70240 ID ADB70240 standard; protein; 720 AA.
 XX AC ADB70240;
 XX DT 04-DEC-2003 (first entry)
 XX C. neoformans amino acid sequence SEQ ID NO:3284.
 XX KW fungicide; gene therapy; infection.
 XX OS Cryptococcus neoformans.
 XX PN WO2003052076-A2.
 XX PD 26-JUN-2003.
 PP 17-DEC-2002; 2002WO-US040225.
 XX PR 17-DEC-2001; 2001US-0341261P.
 PA (ELIT-) ELITRA PHARM INC.
 XX PI Zamudio C, Eroshkin AM;
 XX WPI; 2003-533017/50.
 DR N-PSDB; ADB69157.
 XX PT New nucleic acid, useful for preparing a composition for treating an
 PT infection caused by Cryptococcus neoformans.
 XX PS Claim 9; SEQ ID NO 3284; 136pp; English.
 XX CC The invention relates to a novel purified or isolated Cryptococcus
 CC neoformans nucleic acid molecule comprising a sequence encoding a
 CC polypeptide comprising a sequence not given in the specification. A
 CC polynucleotide of the invention has fungicide activity, and may have a
 CC use in gene therapy. The nucleic acid is useful for preparing a
 CC composition for treating an infection caused by Cryptococcus neoformans.
 CC The present sequence represents a C. neoformans sequence of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/patent/pat_sequences.
 XX Sequence 720 AA:
 SQ

Query Match 46.1%; Score 1658; DB 7; Length 720;
 Best Local Similarity 48.1%; Pred. No. 1.5e-106;
 Matches 335; Conservative 97; Nismatches 176; Indels 88; Gaps 13;

Qy 38 QAQPAGGYONYQGYGQOGGYYQYQNPAGYQQQYQYQYQYQYQYQYQYQYQYQ 97
 Db 48 QQQPFDPY-----GQQGGYQYQG-----QYQGGQGYPQYQYQYQYQYQ 86

Qy 98 RGNYKFNFTNNNNLQXA-----GFOFOQGMSLNDFOQKQOAPKPKTTLKLV 148
 Db 87 -----QGPVPSGAGPRAYGP-PQRNVPFQPPSFSSSPAPPDTKA 132

Qy 149 SSGIKLA---NATKVKUTPKPAESDKKEEKSAAETKEPKPEPTVPEPKKEE -- -KPIQ 201
 Db 133 GKPVSLSIGGGAPK---AAPSLSLIEKEASSSKSSPKPAAPTPKDAPPAKSEAASAPPS 189
 Qy 202 TEKTEKESELPKVEDLK-----I-SESTHTNTNANTV-----AD 236

Db 190 AAEKCAEKA-VPLTSDAQKVVAETSAASPAKGGASTPVATVSTSTTNFSKVSAKNDAE 248
 Qy 237 ALIKEBEEVDFDEVNDMFGG-----KDHVSLIFMGHVDAGKSTMGGNLYLTLGSVDK 289
 Db 249 AIVREQ-NLACDAARDLGYENKDNISHLNIFTGHVDAGKSTMGGOLYLGLGAVDK 307
 Qy 290 RTIEKVEREAKDAGRGWYLSWWMDTNKEERNDGKTLIEVGKAYFETEKREYRTILDAPGK 349
 Db 308 RTMCEKYEQEAKAAGETWYLSWALISGKEERAKAGTIVEVERGRAYFSEKREYRTILDAPGK 367
 Qy 350 MVSSEMIGGSQADVGVLVLSARKCEYETGFERGGTREHALLATQGYNKMKVYVYVNKMD 409
 Db 368 TYVPSMISGAAQADAVLLVLSARKGEFETGEFEREOTREHMLICNGINKLIVVYVNKMD 427
 Qy 410 DPTVWNSKEVYDQCSVNSNFLRAJGYNKTDWVMPVSEYSGANLKDHYDPKKECPWYTG 469
 Db 428 DTRVQNDKGRYDEITTKITPLKAVGFPKTDITTPVSAQIGENMKDVKKLPADWDG 487
 Qy 470 PTILEYLDTDMNHVDRHINAPFMLPTAAKMKDGLTVEGK1E8GHTKKKGQSTLMLMPNKTAV 529
 Db 488 PSLLBHDNNEIMDNTINAPFMLPSKYNELGTMVKLIESGTYRKGDITLMMMNKRHTV 547
 Qy 530 EIQNQYNETENEVDMAMCGBQVKLRIKGVEEDDIPGFVLTSPKPIKSYTKPVQIAIV 589
 Db 548 EVTGFSEQSEDMQNAFCGDNTRMISGSDRDTIPGFVLTSVQRPVKAUTAFADISFI 607
 Qy 590 ELKSTIAAGTGGSCWVHTAIBEVHIVKLHKLERTCNRSKPPAFAKCGMKVIAVLETE 649
 Db 608 DTKNICPGYSCVLLVHTLAEVSVTSFLHYEKTTRSSKPPQFAKAGMLVSALIETS 667
 Qy 650 APVCVETYQDYPOLGRFTLDRDQGTTIAIGKVKLAB 685
 Db 668 APICTERFEDYKMLGRFTLDRDQGTTIAIGKVKLAB 703

RESULT 9
 ABUJ26050 ID ABUJ26050 standard; protein; 716 AA.
 XX AC ABUJ26050;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #708.
 XX KW Fungicide; cyostatic; essential gene; Aspergillus fumigatus; infection;
 XX cancer; contamination; biofilm; antibody; immune response.
 XX OS Aspergillus fumigatus.
 XX PN WO200286090-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013142.
 XX PR 23-APR-2001; 2001US-0285697P.
 PR 27-APR-2001; 2001US-0287066P.
 PR 05-JUN-2001; 2001US-0295890P.
 PR 09-JUL-2001; 2001US-0303899P.
 PR 31-AUG-2001; 2001US-0316362P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
 XX DR WPI; 2003-093124/08.
 XX PT New purified or isolated nucleic acids of essential genes of Aspergillus
 PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 PT or for treating a non-infectious disease in a subject e.g. cancer.

Disclosure; Page; 175pp; English.

XX The invention relates to novel purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as *A. fumigatus*, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by *A. fumigatus*, or to prevent or inhibit formation on a surface of a biofilm comprising *A. fumigatus*. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of *A. fumigatus* to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of *Aspergillus fumigatus* of the invention

XX Sequence 716 AA;

Query Match Score 1557.5; DB 6; Length 716;

Best Local Similarity 46.6%; Pred. No. 1.4e-99; Mismatches 186; Indels 95; Gaps 18;

Matches 332; Conservative 93; Gaps 186; QPROQAAPVATQA 129

Qy 71 QYNNQQGKQYNNPOGGYQQOQNPOGGRNYKNNYNNNLLQYQAGFQQQSQMSL--- 126

Db 102 NQY---GGXNQHQ---QQQT-----

Qy 127 NDFQKQKQAAQPKPKT-----LKLVSSGKILKLNAT--KVET--KPAESDKKEEKS 177

Db 130 PSAPQPAQTAPKASTASAPVLSIGGASSSAPKTVLTSIGTPSPA-----S 179

Qy 178 ETKEPTKEPTKVEEPVYKKEPKVPTKEEKEPKVSELPKVEDLKIS-----EST 225

Db 180 NTPSGTTTGTDMGSAAADAAKVTASKAETKTERKAAGKSSPTPTASGRSSPGRSSP 239

Qy 226 NTRNANVT--SADALIKEQEEBDEVNDMFG--GKDTHSLIFNICHVDAKSTMGNL 282

Db 240 SRGEGGKTKGRDANAYALEQADDEBTIEYKEKEHNNIVFIGHDAKGSTLGGSI 299

Qy 283 LTGSVDKRTIEKYERAKDAGRQGSLWYMDTNKEERNDGKTEVGRAYFETE---- 336

Db 300 VIGVNDTLETKYKREAKEGRETYLWALDLTNEERAKGKTEVGRGHFKLTQSPG 359

Qy 337 --KRYTILDAPGHKMYVSEMGQASQADYGVLYTSARGEYETGFERGQCTREHALIAK 394

Db 360 PIERHSISLDAPGHKSYVHMGASQADYGVLYTSARGEYETGFERGQCTREHALIA 419

Qy 395 TQGUNKMYVYVNMODPTVNSKERYDQCTSVNSFLRAIGYNTKDPVMPVSGYSGAN 454

Db 420 NTGVRKIIIVVNKMDDPTVNSKRFDECTVKSFLAEALGYK-KDLDTEMPISAQQTG 478

Qy 455 LRDHYDPKCECWYGTPLLEYLDTNNHVDHINAPMLPAAKMKGDTIVBGEKLESHI 514

Db 479 IKDRVPKELAPWYNGBSLLEYLAEMKTTPERNINAPMMF1STKRYDMGTMVEGRLEAGV 538

Qy 515 KKGQSTLMPNPKTAYEIQNINETENEVDMAGCQEOKR1KRGVEEDISPGFVLTSPQ 574

Db 539 KKNATCIMMPNRTKVEIAALYGETEDEIATATCGDQVRMRLRGVEEDILPGFVLCSPKR 598

Qy 575 PIKSYTKEVAYQAIAYEIKLSIANGFSCYMHVTAIEYHIVKULHKLKEKGTRNSKKPPA 634

Db 599 LVHCVSAFFAKIRIELKNILTACYCNMHVSAVEETFAALHCKCBEQTGRSRKRPBP 658

Qy 635 FAKGKMKVTA---VLTETAPCVETYDQYDPLGQRFTELDQGTTIAIGKIVKI 683

Db 659 PASQQTIAFLARLEVISSAGAVCYVEREFDYNQMRERFDQGTTAIGMTKL 710

RESULT 10

ABJ25450 standard; protein; 712 AA.

XX ID ABJ25450

AC ABJ25450;

XX DT 16-APR-2003 (first entry)

XX DE *Aspergillus fumigatus* essential gene protein #108.

XX KW Fungicide; cyostatic; essential gene; *Aspergillus fumigatus*; infection; cancer; contamination; biofilm; antibody; immune response.

XX OS *Aspergillus fumigatus*.

XX PN WO200286090-A2.

XX PD 31-OCT-2002.

XX PP 23-APR-2002; 2002WO-US013142.

XX PR 23-APR-2001; 2001US-0285697P.

PR 27-APR-2001; 2001US-0287066P.

PR 09-JUL-2001; 2001US-0303890P.

PR 31-AUG-2001; 2001US-0316362P.

PA (ELIT-) ELITRA PHARM INC.

XX PI Jiang B, Tishkoff D, Zamudio C, Eroszhkin AM, Hu W, Lemieux SM;

XX DR WPI, 2003-093124/08.

XX PT New purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*, useful for treating or preventing infections by *A. fumigatus*, or for treating a non-infectious disease in a subject e.g. cancer.

XX PS Disclosure; Page; 175pp; English.

CC The invention relates to novel purified or isolated nucleic acids of essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as *A. fumigatus*, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by *A. fumigatus*, or to prevent or inhibit formation on a surface of a biofilm comprising *A. fumigatus*. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of *A. fumigatus*, useful to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to

2 EUEPILVENGETMSPBESWEHKEEISSEAEP --GGSLGDGRPPESAHMMEEBEP 58
 247 DDEVVNDMFRG -KDTYSLIFMGHVDAGKSTMGNLILYLTGSVDRKTEKEYEREAKDAGR 304
 Qy 59 KPKSVVAPGAKPKHEVNVVFLGHVDAGKSTGGQIMLYTGMVDRKTEKEYEREAKEKNR 118
 Db 305 QGWLISMVMDTNEERDGTTEVKAYFETEKKRTTLDAGHKNYSEMIGGASQADV 364
 Qy 119 ETWYSLWALDTNQEEKDKGKRTVEGRAYFETEKKHFTILDAGHKSPVPMIGGASQDL 178
 Qy 365 GVLVISARKGKGYETGPERGGOTREHALAKTOGYNRMVWVNNKMDOPTWNSKERYDQCV 424
 Db 179 AVLVISARKGKGYETGPERGGOTREHALAKTAGVHLVILNMDOPTWNSNERYECK 238
 Qy 425 SNVSNFLRAIGYNIKCDVVFMPVSGSGANLKDHDVPECPWYGTPLXLYDTNHNVDR 484
 Db 239 EKLVPPLIKVFSFNPKCDIHMPCSGLTGANLKEQSD -FCFWYIGLPFPIYLDNLPNFR 296
 Qy 485 HINAPPMLPIAARKMDGLTVEGKIESGHKKGQSTLMPNPKTAVEIQNQYNETENEVM 544
 Db 297 SDVGPIRLPLIVDVKYKDMGTVVGLKLESSSTICKGQQLVMMENKHNVEGLGILSD-DVETDT 355
 Qy 545 AMCGBQYKLRKGVEEDISPGFVLTSPKNIKSVTKFVQIAVTEYLKSLIIAGFSCVMH 604
 Db 356 VAPGENLKRURKGIEBELLPGFILCPNNLCHSGRTFDAGIVTEHKSTICPGNNAVLH 415
 Qy 605 VHTAIREVHVYKLLKLEKGTNMRKSKKPPAFAKGKMKVIALETAAPCVETYQDYPOLG 664
 Db 416 IHTCLBEVEITALICLUVKSKGEKSXTRPREVKQDQVCIARLRTAGTICLUETFKDQPMG 475
 Qy 665 RFTLRDQGTTAIGKVKI 683
 Db 476 RFTLRDQGTTAIGKVKL 494

PT erythematous, rheumatoid arthritis, diabetes mellitus or asthma and in
 PT stimulating an immune response.
 XX
 PS Claim 1; SEQ ID NO 280; 309pp; English.
 XX
 CC The present invention describes an isolated PRO nucleic acid (1). Also
 CC a vector comprising (1); (2) a host cell comprising the
 CC vector of (1); (3) a process for producing a PRO polypeptide; (4) an
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
 CC antibody which specifically binds to a polypeptide of (4); (7) a
 CC composition of matter comprising a polypeptide of (4), an agonist or
 CC antagonist of the polypeptide or an antibody that binds to the
 CC polypeptide in combination with a carrier; (8) an article of manufacture
 CC comprising a container, a label on the container and a composition of
 CC comprising (7); (9) a method of treating an immune related disease in a
 CC mammal; (10) a method for determining the presence of a PRO polypeptide
 CC in a sample suspected of having the polypeptide; (11) a method of
 CC diagnosing an immune related disease or an inflammatory response
 CC in mammal; (12) a method of identifying a compound that inhibits or
 CC mimics the activity of or expression of gene encoding PRO polypeptide
 CC; and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have antiallergic, antianemic, antiarthritic,
 CC antiasthmatic, antidiabetic, antinflammatory, antipsoriatic,
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
 CC haemostatic, hepatotoxic, immunosupulant, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC viricide activities, and can be used in gene therapy. The nucleic acid
 CC (1) and the encoded polypeptides compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO protein from the present invention.
 XX
 SQ Sequence 499 AA;

Query	Match	Score	DB	Length
Qy	37.7%; Best Local Similarity Matches 262;	1354.5; Pred. No. 1.e-85;	8;	499;
Db	2 ELSBPVNGETEMSPESWHEKEESEAEP--GGGSLGDRPPESAHMMEEBEP	139;	Indels 9;	5;
Qy	188 KVEEP-VKKEEKPVQTEKEPEKSEPKVPELKLISESTHTNNNANTSADALIKEQEEV 246	58	;	;
Db	247 DDEVVNDMFGG -KDHVSLIPLMGHVDAGKSTGMGNLILYLTGSVDRKTEKEYEREAKDAGR 304	59	;	;
Qy	59 RPKSVTAPPGAPKKBHVNVFIGHDAGKSTGMGNLILYLTGSVDRKTEKEYEREAKEKNR 118	305	;	;
Db	305 QGWLISMVMDTNEERDGTTEVKAYFETEKKRTTLDAGHKNYSEMIGGASQADV 364	119	;	;
Qy	365 GVLVISARKGKGYETGPERGGOTREHALAKTOGYNRMVWVNNKMDOPTWNSKERYDQCV 424	365	;	;
Db	425 SNVSNFLRAIGYNIKCDVVFMPVSGSGANLKDHDVPECPWYGTPLXLYDTNHNVDR 484	179	;	;
Qy	425 EKLVPPLIKVFSFNPKCDIHMPCSGLTGANLKEQSD -FCFWYIGLPFPIYLDNLPNFR 296	485	;	;
Db	485 HINAPPMLPIAARKMDGLTVEGKIESGHKKGQSTLMPNPKTAVEIQNQYNETENEVM 544	297	;	;
Qy	545 AMCGBQYKLRKGVEEDISPGFVLTSPKNIKSVTKFVQIAVTEYLKSLIIAGFSCVMH 604	545	;	;
Db	545 VHTAIREVHVYKLLKLEKGTNMRKSKKPPAFAKGKMKVIALETAAPCVETYQDYPOLG 664	356	;	;
Qy	605 VAPGENLKRURKGIEBELLPGFILCPNNLCHSGRTFDAGIVTEHKSTICPGNNAVLH 415	605	;	;
Db	605 IHTCLBEVEITALICLUVKSKGEKSXTRPREVKQDQVCIARLRTAGTICLUETFKDQPMG 475	416	;	;
Qy	665 RFTLRDQGTTAIGKVKI 683	665	;	;
Db	665 RFTLRDQGTTAIGKVKL 494			

RESULT 14
 ADP54304 standard; protein; 499 AA.
 XX
 AC ADP54304;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human PRO protein sequence SEQ ID NO:280.
 XX DE human; PRO; immune related disease; inflammatory immune response;
 KW immune response stimulation; antiallergic; antianemic; antiarthritic;
 KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
 KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
 KW haemostatic; hepatotoxic; immunosupulant; immunosuppressive; muscular;
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 KW viricide; gene therapy.
 XX OS Homo sapiens.
 PN WO2004039956-A2.
 XX PD 13-MAY-2004.
 XX PP 28-OCT-2003; 2003WO-US034381.
 XX PR 29-OCT-2002; 2002US-0422472P.
 XX PA (GETH) GENENTECH INC.
 XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, William PM;
 PI Wood WI, Wu TD;
 XX DR 2004-376182/35.
 XX DR N-PSB; ADP54303.
 PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
 and treating an immune related disease, e.g. systemic lupus

Db	476 RFTLRDEGGKTAIGKVLC	494	Best Local Similarity Matches 262; Conservative 89; Mismatches 139;	Pred. No. 1.2e-85;	Indels 9	Gaps 5;
RESULT 15						
ID	ADP24765		QY	188 KVEEP-VKKEEKPVQTEEKTEERSPELKVEDLKESTEINTNNANVTSADALIKEQEEEV 246		
XX	ADP24765 standard; protein; 499 AA.		Db	2 ELSESETVENGETENPEESWEHKEEISEAEP--GGGSLGDRPPEESAHMMEEEETP 58		
AC	ADP24765;		QY	247 DDEVNDMFRGG--KDHSVLFMGEVDAGKSTMGNLLYLTSVDKRTIEKVERAKDAGR 304		
XX			Db	59 KPKSVTAPGAPKKEHVNVVFIGHDAGSTIGQQIMVITGMVDKRTLEKVERAKEKNR 118		
DT	18-NOV-2004 (first entry)		QY	305 QGWLTSWMDTNKSERNDGKTTIEVGKAYFETEKRTYTLDAKGKMYMSEIMGGASQADV 364		
XX	PRO polypeptide SEQ ID NO:1943.		Db	119 BTWYISWALDTNQERDKGKTTIEVGKAYFETEKRTYTLDAKGKSFVNMGASQADL 178		
KW	PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; anti-allergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.		QY	365 GVLVTSARKEGEYENCPERGGQTREHALAKTQGYNKOMVYVNNKDDPITNWSKRYDQCV 424		
KW	Unidentified.		Db	179 AVLYTSARKEGEFETCFEXKGQTREHALAKTAGYKHLIVLNQMDPITNWNSNRYEECK 238		
XX			QY	425 SNVSNPFLRAIGYNTKTDVVFMPVSGYSGANLKDHDVDPKCPWTTGPTLLESDYLDTMNHVDR 239		
OS			Db	EKLVPLKVKGFNPKFDIHPMPCSGLTGANLKEQSD--FCPWYIGLPFIPYLDNLPNFNR 296		
XX	WO2004041170-A2.		QY	485 HINAFPEMLPIAAKMKDGLTIVEGKLESHIKKGOSTLIMPNKTAVEIQNLYNETENEVDM 544		
PD	21-MAY-2004.		Db	297 SVDGDIRLPLVDKYRDMGTVLGLKJESGTSICKGQOLVMMENKHNVEVLGILSD-DVETDT 355		
XX			QY	545 AMCGBQVKLRIKGVBEEDISPGEVLTSPQNPIKSVTKFVAQIAVLEKSLTIAAGFSVYH 604		
PF	30-OCT-2003; 2003WO-US034312.		Db	356 VAPGENKLRLKGTEEEELPGFTLCPNWLCHSGRTFDAQVIEHKSTICPGYNAVLH 415		
XX			QY	605 VHTABEVHVKLHLKLEKGTNRKSKKPPAPAKKGMKVIAVLETAAPCVCTYQDYPQLG 664		
PR	01-NOV-2002; 2002US-0423394P.		Db	416 IHTC1EEVEETALICLVDKSGEKSCTRBRFVXQDQVCIARLRTAGTICLETFXDFPQMG 475		
XX			QY	665 RFTLRDQGTTIAIGKIVK 683		
PA	(GETH) GENENTECH INC.		Db	476 RFTLRDGEKTAIGKVKL 494		
XX			QY			
Clark H., Schoenfeld J., Van Lookeren M., Williams PM, Wood WI;			QY			
PI			QY			
WU RD;			QY			
XX			QY			
WPI: 2004-419628/39.			QY			
DR	N-PSDB; ADP24764.		QY			
XX	New PRO polypeptides and polymucleotides, useful for treating e.g. erythemas, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.		QY			
XX			QY			
PS	Claim 7; SEQ ID NO 1943; 2940pp; English.		QY			
XX	The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, anti-allergic, antiasthmatic, hepatotropic, and respiratory activity. A PRO polypeptide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.					
XX	Sequence 499 AA;		QY			
SQ	Query Match		QY			

Search completed: July 1, 2005, 18:16:58
Job time : 197.103 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	30	817	22.7	460	2	T432677
OM protein - protein search; using sw model		31	814.5	22.7	460	2	JC4214
Run on:	July 1, 2005, 18:06:15 ; Search time 40.0283 Seconds	32	813.5	22.6	460	2	T47258
Title:	US-09-591-632-2	33	812	22.6	444	2	T44963
Perfect score:	3594	34	808.5	22.5	461	2	T43704
Sequence:	1 MSDSNQNNQNYQYSQNG.....FTLRDGTTIAIGKVKIAE 685	35	806.5	22.4	446	2	S16308
Scoring table:	BLOSUM62	36	802	22.3	459	2	S59595
	Gapop 10.0 , Gapext 0.5	37	800	22.3	460	2	T43894
Searched:	282416 seqs, 96216763 residues	38	799.5	22.2	449	2	S08534
Total number of hits satisfying chosen parameters:	282416	39	798.5	22.2	448	2	S08507
Minimum DB seq length: 0		40	798.5	22.2	449	2	S06724
Maximum DB seq length: 2000000000		41	798.5	22.2	967	2	F86214
Post-processing: Minimum Match 0%	Maximum Match 100%	42	798	22.2	437	2	C72570
	Listing first 45 summaries	43	797.5	22.2	458	1	EFBYA
Database :	PIR 79.4	44	797	22.2	462	2	A60491.
	1: Pir1.*	45	796.5	22.2	1	EPH01	
	2: Pir2.*						
	3: Pir3.*						
	4: Pir4.*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
	SUMMARIES						
Result No.	Score	Query	Match	Length	DB	ID	Description
1	3594	100.0	685	1	EFBYS2		suppressor 2 protein - yeast (Saccharomyces cerevisiae)
2	2177	60.6	741	2	S12921		N; Alternative names: Gl1-to-S transition protein; protein YDR172w
3	1719	47.8	729	2	T51896		C; Species: Saccharomyces cerevisiae
4	1689	47.0	662	2	T41442		C; Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004
5	1679	46.6	662	2	T41948		C; Accession: S00733; MUID:88172803; PMID:1280807
6	1375	38.3	614	2	S58444		A; Reference number: J0323; MUID:88329727; PMID:3047009
7	1354.5	37.7	499	2	S06941		A; Molecule type: DNA
8	1283	35.7	515	2	T03717		A; Residues: 1-685 <RKS>
9	1213.5	33.8	573	2	T23102		A; Cross-references: EMBL:246727; NID:9172789; PIDN:CAA86677.1; PID:9172791
10	1160.5	32.3	409	2	T03718		R; Murphy L.; Harris, D. B.
11	946.5	26.3	280	2	T43011		Submitted to the EMBL Data Library, November 1994.
12	859.5	23.9	435	2	A49171		A; Reference number: S49764
13	847	23.6	441	2	S54734		A; Molecule type: DNA
14	844	23.5	456	2	S11665		A; Residues: 1-685 <RKI>
15	836	23.3	449	2	A54760		A; Cross-references: GB:Y008859; NID:93711; PIDN:CAA68760.1; PID:93712
16	833	23.2	458	2	S35894		C; Genetix
17	831	23.1	458	2	A3154		A; Gene: SGD:S00735; S00736; S00737; S00738; S00739; S00740
18	829	23.1	458	2	S06300		A; Cross-references: SGD:S0002579; MIPSYDR172w
19	829	23.1	460	2	S35772		A; Map position: 4R
20	828.5	23.1	449	2	JC5117		C; Superfamily: superfamily 2 protein; translation elongation factor Tu homology
21	826	23.0	435	2	S43507		F; 124-255/Domain: charged <DOM2>
22	825.5	23.0	458	2	S43861		F; 1-123/Domain: A
23	825	23.0	460	2	S43861		F; 42-119/Region: 10-residue repeats
24	823	22.9	460	2	T41617		F; 159-222/Region: glutamic acid/lysine-rich
25	822.5	22.9	457	2	S35986		F; 254-685/Domain: C <DOM4>
26	822	22.9	460	2	T38220		F; 261-409/Region: nucleotide binding factor Tu homology <ETU>
27	821	22.8	435	2	H90162		F; 267-274/Region: nucleotide binding motif A (P-loop)
28	821	22.8	459	2	JC4253		F; 406-405/Region: GTP-binding NQXD motif
29	819	22.8	460	2	T42089		

A; Crosses-references: EMBL:ALJ391572; GSDB:GN00116; NCSP: B23111.80	
A; Experimental source: BAC clone B23111; strain OR74A	
C; Genetics:	
A; Gene: NCSP:B23111.80	
A; Map position: 6	
A; Introns: 111/1; 711/3	
C; Superfamily: Suppressor 2 protein; translation elongation factor	
Query Match	47.8%; Score 1719; DB 2; Length 729;
Best Local Similarity	49.9%; Pred. No. 1.3e-81;
Matches 365; Conservative 98; Mismatches 204; Indels 6	
Qy 7 GNNQNYQ------QYSQNGQQGNRNYQYQAYNA-----	
Db 3 GNVQNNWEEAADODERLARQTQQMNINAGTFR PGAAAFTPGABSFTPQQ	
Qy 38 -QAOQAGGYYQYONY-QGYSQYQCGQYQYNPDAQYQOQYNNPQGGYQQYNPQG	
Db 62 YQQYTGAAQGGGGGQYGGGGQYQGQYNNQ--QCGQYGAVYGGCGYNG	
Qy 96 GGRGNY-KNFTNTNNLQCYQAGFQPOSQGMSLND--FOQOKQOQAPK--	
Db 120 QCGGGQCONQGTCQROQCNRDAPKAPAPOLVQRPQPAQPKADAPKTA	
Qy 145 ----KLVSSGIRKLANATKVK--GTRPAESDKEEEKSATETKEPTKEPT	
Db 180 GDAPAKVLSIGGDAKPKAAKVLISIGTAPK--KEEPKEAKKEKGTA	
Qy 197 EKPVQTEKTEKSEKSELPKVEDLKTISBETHNTNNANVNTSADALIKE-QEEEV	
Db 237 QK--TESAAASGRTSPAPSSGRASPSAAKSGNKKVSRDVAVEKDIQSADY	
Qy 256 GGDHDYSLIIFMGHVDAGKSTMGGNLLYLTGSUDKRTIKEYREAKDAGROG	
Db 294 -GKEHNNNIFIGHVDAGKSTLGAIIYLTGMDVDTLTDYKREAKDGMGRT	
Qy 316 NKEERNDGKTTIEVGKAYFETEGRTYTLDAPIGHHRMYSMEIGGASQADYGV	
Db 353 TNEEERAKGKTVTVEGRGFFETDKEKYSILDAPIGHATYVPAHIGGASQADYGI	
Qy 376 YETGEERGGOTPEHALLAKTQCEUNKMYVYVNNKDDPPTVNNWSKBYDQCVSN	
Db 413 YETGEERGGOTPEHALLAKTQGYNKLVYVNNKDDPPTVNNWSSEERYKECTTK	
Qy 436 YNIKTDVVFMPVSGYSGANLKDHDVDPKCPWYGTPLIYLYLDTNNHVDRI	
Db 473 YNLKTDVVFMPVTAQQTMGKIKRVPKDLCPCPWYDGPSSLLEYLDNNMSLRLERKV	
Qy 496 ARMKDGTIVEGRKIESGHKKCOSTLMPNKTAVEIQNQTYNETENEDMAM	
Db 533 GKYRDNGTMIEKSKIEAGVTKKGMSLIMMPNQKQSBISAYVGETDEPVYAQ	
Qy 556 KGVEEDEIDSPGVLTSKPNPIKSYTKEFQIAQIAVELKSTIAAGFSCVMMTH	
Db 593 RGIEEEELIMPGGVLCSPKRLVHNTAFAQIRILDLKSILTAGTNCVCLHVFH	
Qy 616 KLLHKLKEGTNPKNSKKEPPAFAKGKMGKVIAVLET--EAPVCVTYQDYPOL	
Db 653 ALLHKLQKGTNPKNSKLPFSHAKKGDSIARLEVTTGGAGSVCFERFEDYQFM	
Qy 673 TTAIAIGKIVKI 683	
Db 713 QTAIAIGKIKTL 723	

RESULT 5
T51948
omnipotent
C; Species
C; Date: 2
C; Accession

A; Reference number: 221993		A; Accession: T41442	
A; Status: preliminary; tra		A; Molecule type: DNA	
A; Residues: 1-662 <SEE>		A; Cross-references: UNIPRO	
A; Experimental source: str		A; Experimental source: str	
C; Genetics:		A; Gene: SPDB:SPCC584.04	
A; Map position: 3		A; Map position: 44/1	
C; Superfamily: suppressor		A; Introns: 44/1	
F; 239-387/Domain: translat		C; Superfamily: suppressor	
Query Match			
Best Local Similarity		Conservat	
Matches 342;		Conservat	
Qy	4	SNGQNNQNYQQ	
Db	3	SNGQNNNGQEQQ	
Qy	64	NPDAGYQQQYNP	
Db	51	N-----N	
Qy	122	QGMSLN-----	
Db	86	TGNTVDEDKSRL	
Qy	157	ATKVGTRPAAESI	
Db	146	TRPAA--PAAQG	
Qy	217	DLKISESTHTNN	
Db	199	AAALKRKAABAAE	
Qy	277	GGNLILYLTSSVVD	
Db	255	GGNLILFLTGMDV	
Qy	337	KRYTTLDAFGH	
Db	315	HRFLSLLDAFGH	
Qy	397	GVNKMVVYVYNNKMI	
Db	375	GINHLLVVVYNNKMI	
Qy	456	KDVTDPKCECPWY	
Db	435	KDRVDSVCPWY	
Qy	516	KGOSTLILMENKTY	
Db	495	KNSNLVLPMPINQ	
Qy	576	IKSVTKFVQIA	
Db	554	VPTPTTRFIAQIA	
Qy	636	AKXGMKVTALEV	
Db	613	ATRGMKIAAEL	

R;Ito, K.; Ebihara, K.; Nakamura, Y.
RNA 4, 958-972, 1998
A;Title: The stretch of C-terminal acidic amino acids of translational release factor eRF3
A;Reference number: Z25983
A;Accession: T51948
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-662 <IT0>
A;Cross-references: UNIPROT:074718; PIDN:D79214; EMBL:BAA3530.1
A;Experimental source: strain JY333
C;Genetics:
A;Gene: Sup35
A;Introns: 4/1
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology
Query Match Score 1675; DB 2; Length 662;
Best Local Similarity 47.9%; Pred. No. 2.1e-79;
Matches 340; Conservative 121; Mismatches 171; Indels 78; Gaps 17;
Query 4 SNOGNNQOQQYSONGNNRQYQGQAYNAQAOQACGYYQNYQGSGYQOGGQYQ 63
Db 3 SNNQPNQGQDQBLQKTSMSAKAPTPKAAPFIPS-----FQPGFV 50
Query 64 NPDAGYQQQYNPQGG-XQDYNPQGGYQQQFNPNPQGGRNQKKNFVNYYNNLQGQAFQPOS 121
Db 51 N-----NIAQGXYPAQXTGQG-----QNSNSPHPTKSYLYYQ-KP 85
Query 122 QGMSLN-----DQPKQKQAAPKPK-----KTKL-----VSSSGIQLAN 156
Db 86 TGNTVDEDKSRSVPDFSKKSFVPPKPAIPKGKVLSLGGNTSAPKSTKPPISISLGGTAKF 145
Query 157 ATKKVGTKPAESDKKBEKEAETKEPTKEPTKVEBPKVKEEKPVKEPTKEETKEKSELPKVE 216
Db 146 TTKPAA-PAQSKTETPKVTSSESTKETAAAPP---QETP-TKSDAELAKTPSP 198
Query 217 DLKISESTHTNNNANTSADALIKEQEEEVTDDEVNDMFGKDHVSLIIFMGHVDAGKSTM 276
Db 199 AAALKKAEEAEEAPVTE-DA-TDQNQEYDQELKDMV GKEHVNIVITGHVDAGKSTL 254
Query 277 GGNLILYLTGSVDKRTIEKYBREAKDAGRQEWYLSPVMDNTKEENDGKTEVKGAYFETE 336
Db 255 GGNLILYLTGSVDKRTIEKYBREAKDAGRQEWYLSPVMDNTKEENDGKTEVKGAYFETE 314
Query 337 KRRYTTILDAPGHKMYVSEMGQASQADYCVLVISSARIGBEYETGPERGGOTREHALAKTQ 396
Db 315 HRRFSLDAPIHKGVTVNMINGASQDIDGVLVISARRGFBAGFRGGQREHALAKTQ 374
Query 397 GVNKMYVYVNMKMDPTVNSKERYDOQCVSNVSFLRAI-GYNIKTFDVFMPVSGYSGANL 455
Db 375 GINHLYVVTNMDPEPVQNSVSEERYKECDVLSMPLRRAVGSNSKTDVKMPVSAVTQGTV 434
Query 456 KDHVDPKCPYPTGPFLLYDIDTMNHVDRHINAPMPLTAAKMDLGTVEKGKESGHIK 515
Db 435 KDRVDSSSVCPYPTGQSLVLEEDSMTHLERYKVNAPYIMPAKYDGLTLEKGKLEAGSK 494
Query 516 KGQSTLMLPNTKTAEVQNTYNETENEDVAMCGBQYKLKGVVEFEDISFGFVLTSPKNP 575
Db 495 KNSNVLMPINQTLTAYDEAIISSCGDVRLRVORG-DSDSVTQGVLTSTKNP 553
Query 576 IKSUTKPVFAQTAIVELKSIIAAGFSCVMWHTAEEVHIVKLHLEKGTNRSKPKPAP 635
Db 554 VHAUTRFIAQTAIELPSLTTGYSVCMHHTAVEGVSARLHQLDK-TNRSKPKPMP 612
Query 636 ARKGKMKVIAVLETAPEAVCVTYQDFQLGRETFLRDQGTTAIGKVKVIAE 685
Db 613 ATKGMKIIAELLETQTPVCMERFEDYQMGRETFLRDQGTTAVGKVKVILD 662
Db 495 KNSNVLMPINQTLTAYDEAIISSCGDVRLRVORG-DSDSVTQGVLTSTKNP 553
Query 576 IKSUTKPVFAQTAIVELKSIIAAGFSCVMWHTAEEVHIVKLHLEKGTNRSKPKPAP 635
Db 554 VHAUTRFIAQTAIELPSLTTGYSVCMHHTAVEGVSARLHQLDK-TNRSKPKPMP 612
Query 636 ARKGKMKVIAVLETAPEAVCVTYQDFQLGRETFLRDQGTTAIGKVKVIAE 685
Db 613 ATKGMKIIAELLETQTPVCMERFEDYQMGRETFLRDQGTTAVGKVKVILD 662
RESULT 7
S06341 suppressor 2 protein homolog - human
N;Alternate names: GST1 protein homolog
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S06941
R;Hoshino, S.-I.; Miyazawa, H.; Enomoto, T.; Hanacka, F.; Kikuchi, Y.; Kikuchi, A.; Ui, M
EMBO J. 8, 3807-3814, 1989
A;Title: A human homologue of the yeast GST1 gene codes for a GTP-binding protein and is
A;Reference number: S06941; PMID:9005983; PMID:2511002
A;Accession: S06941
A;Molecule type: mRNA
A;Residues: 1-499 <HOS>
A;Cross-references: UNIPROT:P15170; EMBL:CAA35635.1; PIDN:931920; NID:931920; PID:931921
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
RESULT 6
S58444 protein - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

Best Local Similarity 49.6%; Pred. No. 2.8e-50;							
Matches 254; Conservative 89; Mismatches 148; Indels 21; Gaps 7;							
Qy	185	EPTKVEPVKKB	---BKPVOTEKEPKRSELPKVEDLKRKISEETH	-----NTNNAVNTS	234		
Db	5	EDGDBEAKIPEKTKEDS	MAEEGAGDDEKDPIDPEDELKRAHDPLEPKVKGIA	G	64		
Qy	235	ADALIKEQEEFDEV	-VNOMFGGKDHSVSLI	FMGHVADKGSTMGGNNLULTGSDVTKRTIE	293		
Db	65	KEA	--SPPEDQIDEV	VNK	--KRHLNVVNEIGHDAGKSTIGQILLLSQVQDRTIQ	117	
Qy	294	KYEREAKDARQGWILSWMDNTKNEKENDGKTEV	GKAYFETEKRTTILDAPKHMVTS	353			
Db	118	KYEREAKDKNRRESW	TMAYI	MTNEEERVKGTTEVEGRAHFETDTTRFTILDAPGHSKSYVP	177		
Qy	354	EMIGGASOADVGVLYTISARK	KEYETGFERGGOTREHALLAKTOFGVNQKVWVYNNRMDPFTV	413			
Db	178	NMISERSQADIGLITISARK	KEFETGFERGGOTREHQLARTLGVTKEVLLVQVNNRMDPFTV	237			
Qy	414	NWSKERYDOCVSNVSNFLRAGYNTIKTDDVYFMPVSGYSGANLKDHDVDPKECPKHYTGPTUL	473				
Db	238	NWSKERYDETEISKMVPFLRSGYNTKDDVQFLPISGPNWNGKESVCPWNGPCLF	297				
Qy	474	EYLDTMNHYDRHINAPFLMLPAAMKQDGLTGIVTEVGK	ESGHIKKGOSTLMLMPNKTAVELION	533			
Db	298	ETLDAVEVPRDPNGPLRMLPDKFQDMGTVYMGKE	ESGSIHEGDNLLIIPNKAAYKVLA	357			
Qy	534	YNETENEVDMAMCGEQVKLRLKGVEBEDISPGFVLTSPKNP1KSVTKPKVQAIVEL	--	591			
Db	358	IFCD-EDKVRHVPGGENVRVLSGVPGEDDIUSGFVLSVAKP1HAVENTEVAQOLILELLJD	416				
Qy	592	KSIIAAGFSCSTMVHTAIEYTHVVKLHLKEGKTNRKSKKPPRAFAKGKGMKVIAVLETEAP	651				
Db	417	NAIFTAGYKAVLHTHSVECEBIVLMQDILKTKPCKMKKKPLFVNGAIVLCRVQVNRL	476				
Qy	652	VCVETYQDYLQGRFTLDRQGTTIAKGIVKI	683				
Db	477	ICVEKFSDFAQLGRFTLRTBEGTKVAVGKITAL	508				

Qy	210 SELPKVEDDLKISESTNTNNANVTSADALIKEQEEBVDDEEVNDMFGGGDKDHVSLJFMGTV 269	Db	125 KMDDPDTVNSKERYDEIESKMPPLRSSTCNVCKDVKPLISGNSNLKTRMEKSVCNW 184
Db	97 ----RTVVDGGH-----	Qy	467 YTGPITLEYDMDTMDVDRHINAPMPLIAAKMDLGTVEGKLESHIKKGQSTLMPNK 526
Qy	270 DAGKSTMGGENLILYLTGSVDRKTIEKVEREAKDAGRGWYLISWMDTNCERNDGKTIENG 329	Db	185 WNGPCLFETIDAVEVPPRDPNGLPMLIDKFMDGTVMGKTESGSIREGDNLVMPMK 244
Db	119 DAGKSTGGQMLFETGMVDRKTLEKVEREAKERGKRESWTLSCWMDTNDEREKSKTVEG 178	Qy	527 TAVERQNTYNETENEVDMAMCGBEOKVLRKLGKVEBESDIPGFLVTSKPNPIKSVTKEVQAI 586
Qy	330 KAYFETEKRYTILDAGPHKMYVSEMIGASQADGVVILSARKEGYETGFERGQOTREH 389	Db	245 AAVKTLAIFCD-EDKVRHNGPGENVRVLISGVEDDILISGFVLCSVARDIHAVEFVAQL 303
Db	179 RAYFETEKRYTILDAGPHKRSVPMNIVGANOQDIALAVINSARGEFETGFDRGQOTREH 238	Qy	587 AIVEL--KSI1AAGFSCVMHVTAAEYHVKULHLEKGTNRSKKPAPAFAKGKMKVIA 644
Qy	390 ALLAKTQGYNKMMVVVNNKMDDPPTVNSKERYDQCVSNVSNFLRAIGYNTIKTDVVFMPVSG 449	Db	304 QILELDDNAIFTACKYAVLHHSVTECIEVELMQIDLRTKCKMCKPLFVNGAIVLC 363
Db	239 SMLVKTAGVXHLVILNKMDDPVKEEWFKEIEGKLIFPLRGFNPKTDITYVPCSG 298	Qy	645 VLETFAPCVCTYDYPQLGRFTLRDQGTTIAIGKIVKI 683
Qy	450 YSGANLKDHYDPKECPWYTGPTTLEYLDT-MNHYDHRHINAPMFMLPIAAKMDLGTIVEGK 508	Db	364 RVQVNLLCIVKFSDFALQGRFTLRTEGKTVAVSKITAL 402
Db	299 LTGAFIKDRPTGSEGNWSGPCTEFIDVLLPSYKRDFFGVPVRCITVAEYXSEMGTVIICK 358	RESULT 11	
Qy	509 IESGHIKKGOSTLMPNKTAVEIQNNTENEVDMAMCCEQVKURIKGVEEEDISPGTV 568	Db	43011 suppressor protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
Db	359 MESGCVQKGDTLWNPNKQPVQVLOIWAQ-DVTERVAGDNIEFKLKGIEENLQGFI 417	Qy	C;Species: Schizosaccharomyces pombe
Qy	569 LTPSPNPIKSVTKFVQAQIAVELKSLIAAGFSYMHVTAIEYH1-VRLHLKHLKEKG--- 624	Db	C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
Db	418 ICSPSLAKTGRVDEAVLVLERHSLIASGSCVHRIQSAVEETVVKOCLRPBELLGGP 477	Qy	R;Yoshikawa, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
Qy	625 ----TN-----RKS--KKPPAFAKKGKMKVIAVLETE 649	Db	DNA Res. 4, 363-368, 1997
Db	478 IGGITNSGDMWERPQNRLGLOYAHFCNCRTGVIATIDRKTKGEKKRKFVKQDKEKCIMRLSPS 537	Qy	A;Title: Identifier of open reading frames in Schizosaccharomyces pombe cDNAs.
Qy	650 APVCVETYDQYDPLQGRFTLRDQGTTIAIGKIVKAE 685	Db	A;Reference number: Z17323; MUID:98162722; PMID:9501991
Db	538 EPFVLEPFEKEYPYLGRFTLRDGKTIAGKVLKVKVE 573	Qy	A;Accession: T43011
RESULT 10			
T03178	2 protein homolog - common tobacco (fragment)	Db	A;Status: preliminary; translated from GB/EMBL/DBJ
C;Species: Nicotiana tabacum (common tobacco)		Qy	A;Molecule type: mRNA
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004		Db	A;Residues: 1-280 <YOS>
C;Accession: T03718		Qy	A;Cross-references: UNIPROT:P78857; ENSEMBL:D89207; NID:91749621; PID:BA13868-1; PID:g174
R;Branderup, K.A.; Oettström, G.W.; Brunold, C.		Db	A;Experimental source: strain PR45
Plant Physiol. 108, 1748, 1995		Qy	C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology
A;Reference number: Z15026		Db	Qy 405 VNKMDPDTVNSKERYDQCVSNVSNFLR1-GYNKTDYVEMPVSGYSGANLKDHYDPKE 463
A;Accession: T03718		Qy	Db 1 INKMDPDTVNSKERYDQCVSNVSNFLR1-GYNKTDYVEMPVSGYSGANLKDHYDPKE 463
A;Status: preliminary; translated from GB/EMBL/DBJ		Db	61 CPWTGPSLLEYDMSMTHLERKYNAPFIMPLASKYKDLGTILESKIEAGSKNSNLVM 120
A;Molecule type: mRNA		Qy	524 PNTKTAEVIONIYNETENEVDMAMCCEOYKLRIKSGVEEEDISPGFVLTSPPNPKSVTKEV 583
A;Residues: 1-409 <BRA>		Db	121 PINQTLLEVTAIYDAEBSISSLICDQVRLRVRC-DDSDVQTGTVLTSTKNPVETATRFL 179
A;Cross-references: UNIPROT:Q40582; EMBL:L38829; PID:91009233; PID:9100		Qy	584 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
A;Experimental source: strain SR1		Db	180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
C;Genetics:		Qy	Db 180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
A;Gene: SUP2		Qy	Db 180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
C;Superfamily: suppressor 2 protein; translation elongation factor Tu homology		Qy	Db 180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
C;Keywords: GTP binding; nucleotide binding; P-loop		Qy	Db 180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
F;386-393/Region: nucleotide-binding motif A (P-Loop)		Qy	Db 180 AQIALEVLSIIAGFSCVMHVTAAEYHVKLHLKEGTNRSKKEPPAFAKGMKV1 643
Qy	287 VDKRTIKEYEREAKDAGRGWYLISWMDTNEERNDGKTEVKGAYFETEKRRYTLIDAP 346	Db	Db 5 VDDRTIQKEYEREAKDGNRESWYMAIMDNEERVGKTEVGRHFEFTTRFTFLIDP 64
Qy	347 GHKMYVSEMGASQADGVYLIVISARKGKYEETGFERGQOTREHALLAKTQVGNKPVVWN 406	Qy	Db 65 GHKSTVPMNISGASQDGVYLIVISARKGKYEETGFERGQOTREHALLAKTQVGNKPVVWN 124
Db	65 GHKSTVPMNISGASQDGVYLIVISARKGKYEETGFERGQOTREHALLAKTQVGNKPVVWN 124	Qy	Db 387 AVLETFAPCVCTYDYPQLGRFTLRDQGTTIAIGKIVKIAE 685
Db	387 AVLETFAPCVCTYDYPQLGRFTLRDQGTTIAIGKIVKIAE 685	Qy	Db 239 AELETQTPVCMERFEDYQMGRTFIRDQGTTVAIGKVKILD 280
Qy	407 KMDDPTVNSKERYDQCVSNVSNFLRAIGYNTIKDVFMPVSGANLKDHYDPKECPW 466	Qy	Db 407 KMDDPTVNSKERYDQCVSNVSNFLRAIGYNTIKDVFMPVSGANLKDHYDPKECPW 466

A; Reference number: A49171; MUID:93049915; PMID:1385189

A; Accession: A49171

A; Molecule type: mRNA

A; Residues: 1-355 <RAN>

A; Cross-references: UNIPROT:Q04634; GB:D11083; NID:9217407; PID:9217408

A; Note: sequences extracted from NCBI backbone (NCBIN:117509, NCBIPI:117510)

A; Accession: B49171

A; Molecule type: protein

A; Residues: 2-21 <R22>

C; Genetics:

A; Gene: tuf

A; Start codon: GTG

C; Superfamily: translation elongation factor Tu homolog

C; Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis

F; 12-160/Domain: translation elongation factor Tu homology <ETU>

F; 18-25/Region: nucleotide-binding motif A (P-loop)

F; 157-165/Region: GTP-binding NQXO motif

A; Reference number: A49171; MUID:93049915; PMID:1385189
 A; Accession: A49171
 A; Molecule type: mRNA
 A; Residues: 1-355 <RAN>
 A; Cross-references: UNIPROT:Q04634; GB:D11083; NID:9217407; PID:9217408
 A; Note: sequences extracted from NCBI backbone (NCBIN:117509, NCBIPI:117510)
 A; Accession: B49171
 A; Molecule type: protein
 A; Residues: 2-21 <R22>
 C; Genetics:
 A; Gene: tuf
 A; Start codon: GTG
 C; Superfamily: translation elongation factor Tu homolog
 C; Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
 F; 12-160/Domain: translation elongation factor Tu homology <ETU>
 F; 18-25/Region: nucleotide-binding motif A (P-loop)
 F; 157-165/Region: GTP-binding NQXO motif

Query Match 23 68; Score 847; DB 2; Length 441;
 Best Local Similarity 39.2%; Pred. No. 8.9e-37; Gaps 5;
 Matches 168; Conservative 99; Mismatches 154; Indels 8; Gaps 5;
 Query 258 RDHVSLLFPMGHVDAKGSKTGMGLLVLTSVSKRTRTIEKRYEREAQDAGRGWYLSWMDT
 317 9 KPHLNLIVIGHVGDCKSKTWTCHLYRLGYDEKTCVMIIEESKQNGKESKFAWILDRMK 68
 Database 318 BEERNGKTIIEVGKAYFETEKRYRTILDAPGHKMYSEMIGCASQADGVGLVISARKGEYE 377
 69 BEEREGVTLISYMPFETKCYFTTILDAPCHRDFTKMTGASQADAIIUVSARKGEFE 128
 Query 378 TGFERGGOTREHALAKTQGVNKKVWVVKMDDPTVNNSKERYDQCVSNVSNFLRAIGYN 437
 Database 129 AGMSAEQGOTREHALARTGNCINOLIVAINRMDATPPYSEKRYNNEKTELKGKFLKGKGYD
 438 438 IKTDVVFMPVGSYSSANLKDHDVDPKCPWVTPGTLBEYDMDHVRDHINAPFMLPI-A 495
 Database 189 V-SKPFIPISAWTCENLIER-SPNMPWYNGPILVEPPKPKPINKPLRPQDVF 245
 Query 496 AKMKDQGTTVEGKLESGHIIKGQSTLLMPNKTAYEIQNITYNETEN-EVDNAMCGBOKLR 554
 Database 246 YNISSGIVVPGVRYTGVKGDKVMPAGLVAVEVKTI-ETHHTKIEKAEPGGNIGNF 303
 Query 555 IKGVBEEDISPGFVLTSPKPNPIKSVTKFVQIAQIAWELKSLIAAGFSCVMHHTAEEVH1 614
 Database 304 VKGVKEKDKIKGVDGSLDVPPTV/DEFPARIMWHPATAIVGTPVTHVHTASVACRI 363
 Query 615 VRLHLKLEGTNRSKPKPAFKKGKMKVIAVLETPAPVCVETYQDQPLQGFTLBDQGT 674
 Database 364 TEIIKAKDPTGKEIKNPHFLQKQDIAVKEKPKTVPLVYKSFQGLGRFAMDMGKT 423
 Query 675 TAIGKIVKI 683
 Database 424 IGGVLEI 432
 Database RESULT 14
 S11665
 Query translation elongation factor eEF-1 alpha chain - slime mold (Dictyostelium discoideum)
 Database A; Alternative names: actin-binding protein ABP-50
 C; Species: Dictyostelium discoideum
 C; Date: 12-Feb-1993 #sequence revision 13-Sep-1998 #text_change 09-Jul-2004
 A; Accession: S11665; S36934; S36935
 R; Yang, F.; Demma, M.; Warren, V.; Dharmawardhane, S.; Condeelis, J.
 Nature 347, 494-496, 1990
 A; Title: Identification of an actin-binding protein from Dictyostelium as elongation factor
 A; Reference number: S11665; MUID:91015340; PMID:2215665
 A; Accession: S11665
 A; Molecule type: mRNA
 A; Residues: 1-453 <YAN>
 A; Cross-references: UNIPROT:P18624; EMBL:X55973; NID:97274; PID:CAA19443.1; PMID:97275
 A; Experimental source: strain AX-3; clone 50-1.7
 A; Accession: S36934
 A; Molecule type: mRNA
 A; Residues: 7-456 <YAN>
 A; Cross-references: EMBL:X55972; NID:97276; PID:CAA39442.1; PMID:97277
 A; Experimental source: strain AX-3; clone 50-1.5
 A; Accession: S36935
 A; Molecule type: Protein
 A; Residues: 9-17,128-149;162-166;418-421 <YAF>
 C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C; Keywords: actin binding; blocked amino end; GTP binding; nucleotide binding; P-loop; P-loop; P-loop
 F; 11-159/Domain: translation elongation factor Tu homology
 A; Note: the authors translated the initiation codon GTG for residue 1 as Val
 C; Genetics:

F; 17-24/Region: nucleotide-binding motif A (P-loop)

F;156-159/Region: GTP-binding NKXD motif

Query Match 23.5%; Score 844; DB 2; Length 456;

Best Local Similarity 41.0%; Pred. No. 1.3e 36;

Matches 176; Conservative 82; Mismatches 161; Indels 10; Gaps 6;

Qy 258 KDHVSLIFMGHVDACKSTMGGNLLYLTGSYDKTTEKYEREAKDAGRCWYLSWMDTNK 317

Db 8 KTHNIVVCHVDAACKSTMGGNLLYLTGSYDKTTEKYEREAKDAGRCWYLSWMDTNK 317

Qy 318 EERDGKTLBVGAYFETEKKRTYILDAGHMYVSEIGGASADGVYLVISARKEVB 377

Db 65 AEREGITIDIALMKFESPKSVFTIDAGHGRDFIKNMJTGTSQADCAVLVIASPTGE 124

Qy 378 TGFERRGGTREHALAKTOGVNKVYVYVNKMDDPTVNNSKERYDQCVSNVSNFLRAIGYN 437

Db 125 AGISRDGOTPREHALAFTLGVKQNVCCNRMDDDKTVNQGQRVDBIVEVSAVYIKRKGVN 184

Qy 438 IKTDVWEMPVSGYSGANLKDHDPEKCPWYTGPTILEYDLMHVDRHINAPFMLPI - A 495

Db 185 VE-KVRFVPSGQDNME - KSEKMPYKGPPTILEADMLLEPPVRESDKPLRPLQDY 241

Qy 496 AKMDLGLTVEGKLBSGHTRKGQSTLMPNKTAVIEQVYNETENEVDNAMCQEQQVLR 555

Db 242 YKIGGIGTPVGRVBTGUMKPGDVVTFAVANVTEVKSIEMH - QLAETPGDNVGFNV 300

Qy 556 KGVEEDISPGFVLTSPKN - PIKSVTKEVQATIAVELKSLIAAGFSCYMHVHTAEYVH 614

Db 301 KNVSVKDTRGNYCGNTNDPPEADFTAQVILNHPCIQNGYAPVLDCHTSHACKF 360

Qy 615 VKLHKLEGTRNRSKSKPFAKGMKVIAVLETAAPCVETYDQPLGREFLIRDQGT 674

Db 361 AELESKIDERSGKELEAKSKTSKSGDAAVRMYEQPKPVCVEVNDYAPIGRFAVDMRQ 420

Qy 675 IATIGKIVKIAE 685

Db 421 VAVGIKAVTK 431

Search completed: July 1, 2005, 18:20:58

Job time : 42.0283 secs

Qy 672 GTTAIGK1 680

Db 424 RQTVAVGV1 432

RESULT 15

A54760 translation elongation factor eEF-1 alpha chain - *Trypanosoma brucei*C;Species: *Trypanosoma brucei*

C;Accession: A54760; SeqID: C9394

R;Kaur, K.J.; Ruben, L.

J. Biol. Chem. 269, 23045-23050, 1994

A;Title: Protein translation elongation factor-1alpha from *Trypanosoma brucei* binds calmodulin

A;Reference number: A54760; MUID:94364999; PMID:8083206

A;Accession: A54760

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-239; TCT, 243-449 <KAU>

A;Cross-references: UNIPROT:P41166; NID:9507782; PID:AAA57476.1; PID:9507783

R;Baldau, S.L.; Palmer, J.D.

Proc. Natl. Acad. Sci. U.S.A. 90, 11558-11562, 1993

A;Title: Animals and fungi are each other's closest relatives: congruent evidence from mRNA and protein sequence alignments

A;Reference number: A49394; MUID:94089672; PMID:8265589

A;Status: preliminary: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 18-415 <BAL>

A;Cross-references: GB:125868; NID:9438909; PID:AAA16602.1; PID:9438910

C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog

C;Keywords: calmodulin binding; GTP binding; nucleotide binding; P-loop

F;8-156/Region: translation elongation factor Tu homology <ETU>

F;4-21/Region: nucleotide-binding motif A (P-loop)

F;153-156/Region: GTP-binding NKXD motif

Query Match 23.3%; Score 836.5; DB 2; Length 449;

Best Local Similarity 39.9%; Pred. No. 3.2e-36; Mismatches 164; Indels 7; Gaps 5;

Qy 356 IGGASQADGVYLISARKGEYETGFERGOTREHALAKTOGVNRMVWVYNNKMDDPFTVNW 415
 Db 170 IGGASQADLAVLISARKGEYETGFKGQTRHAMFGTAGVRLIVLNKMDDPFTVNW 229

Qy 416 SKERYDQCSVNSNFSNLFRLAIGYNIKTDVYMPVSGSGSAGNLKDHDVDPKCECPWYTGPTLLEY 475
 Db 230 GIERYBECKERLVPFKVGFSPCDIHMPCSGTGANTKEQSD--FCPWYTGFLPFIPIY 287

Qy 476 LDTMHVHDHRHINAPMFLPLAIAKMDGDTIVEGKIESGHIKKGOSTLMLMPNKTAVIQLNY 535
 Db 288 LNNLPNFNSRSLDGPFLPRLPVDKYKDMGTVVYUMLGKLESGSTIKFGQOLVMMPNKHNEVGLI 347

Qy 536 NETENFDAMCGBEVKPLRKIGVEEDISPGFLVSPKNPILKSSTVFKFVAQIAVIELKSTI 595
 Db 348 SD-DRETDFVAPGENILKIRLKGIEEBILPEFILCDPSNLCHSGRTEDQIVIVIEHKSTI 406

Qy 596 AAGFSCSMYHATAEEVHIVYKLHKLEGTNRSKSKPAPAKKGKMKVIAVLETEAPVCVE 655
 Db 407 CPGYNALVLAHTCIEVEITALISLVDKSCBKSCTRPRFKVQDVCIALRRTACTCLE 466

Qy 656 TYQDYQLGRTPLRDQGTTIAIGKVKI 683
 Db 467 TFKDPPQMGRFTLRDQGTTIAIGKVKL 494

Qy 23 1%; Score 831; DB 4; Length 460;
 Db 39 0%; Pred. No. 2.3e-64;
 Matches 173; Conservative 87; Mismatches 160; Indels 24; Gaps 9;

Qy 258 KDHVSLIIFMGHDAKSKSTMGGNLILYLTGSYDVKRTEAKDAGROGNYLSWVMDTNK 317
 Db 7 RTHVNVVIGHVDSRSITTTGHLTYRCGGIDKRTLEKFKEREAEGKGSPPAYWLDKLK 66

Qy 318 BERNDGKTIEVGKAYFETEKRYTILDAPOKHMYVSEMICGASQDVGVLVISAKGHEY 377
 Db 67 AEREGITIDIALMRKFETPKYHVTWDAPGHDRTFKNMLTGTSQDCAITLITAGTGEFE 126

Qy 378 TGFERGGTREHALAKTOGVNRMVWVYNNMDPFTVNSKERYDQVNSNSNFLAIGY 437
 Db 127 AGISRDGQTREHALAIALYTGKVLIVAVNKMD--SVRKWDKRNRFELIKEKTSNFVKKVGYN 184

Qy 438 IKTDVYMPVSGSGANLKDHDVDPK-ECPWY-----TGPFLLEYDPMHNHVDR 484
 Db 185 PKT-TPFVPSGWNNDNM--IBPTNCPYKGMKETKSGVTKTLLPAIDA-BPPTR 240

Qy 485 HINAFMLP1--AAMKMDLGTIVEKQKESHHIKKGOSTLMLMPNKTAVEIQNINYNETENEV 542
 Db 241 PTDKELRLPQDVKYKIGGIGTVPVGRVETLIRAGMVMVTFAPAGYTTEVKSVMH-EQL 299

Qy 543 DMAMGCGEQYKLIRKVEEDISPGFLVSPKNAVQAAIVEKLSSILAGFSC 601
 Db 300 AEGVGDNYGPNVKNVSKEIRRGNVCGDSKNDPKGCDSPNAQIVLNHPGQ1SAGYSP 359

Qy 602 VMHVTAAEEVHIVLHKLEGTNRSKSKPAPAKKGKMKVIAVLETEAPVCVETYQDYP 661
 Db 360 VLDCTIAHACKFDLVEKIDRRTYQKLEENPKFVRSQDAIVRNVPKPMCEAFTDYP 419

Qy 662 QLGRTFLRDQGTTIAIGKVKIAE 685
 Db 420 PLGRPAVDRMQRQTVAVG-VIKSVE 442

RESULT 10
 US-08-299-351-1
 Sequence 1, Application US/08299351
 Patent No. 5576186
 GENERAL INFORMATION:
 APPLICANT: Steiner, Dean A.
 TITLE OF INVENTION: DIAGNOSIS AND MONITORING OF
 TITLE OF INVENTION: RHEUMATOLOGICAL DISEASES BY DETECTION OF ANTI-EP-1-alpha
 TITLE OF INVENTION: ANTI-BODIES
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOVE, WILLIAMS, TIMMONS & COLLINS
 STREET: 1400 Mercantile Bank Tower, 1101 Walnut St.
 CITY: Kansas City
 STATE: Missouri

COUNTRY: USA
 ZIP: 64106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,351
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cleveland Jr., Dan
 REGISTRATION NUMBER: 36106
 REFERENCE/DOCKET NUMBER: 22702
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (816) 474-9050
 TELEFAX: (816) 474-9057
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 462 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 AUTHORS: Uetsuki,
 JOURNAL: J. Biol. Chem.
 VOLUME: 264
 PAGES: 5791-5798
 DATE: 1989
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 462
 US-08-299-351-1

Query Match 22.3%; Score 801.5; DB 1; Length 462;
 Best Local Similarity 38.3%; Pred. No. 9e-62;
 Matches 169; Conservative 90; Mismatches 157; Indels 25; Gaps 8;

Qy 258 KDHVSLIFMGHVDAGKSTMGNNLILYLTGSVDKRTIEKYREAKDAGRGWYLSVMDTNK 317
 Db 5 KTHYNLWVIGHVDAGKSTTGHLIYKCGSIDKRTIEKFKEADELGKGSFKYAVNLDKLK 64

Qy 318 EERNDGKTEVGVKAYFETEKRTYRRTILDAGHCKMYVSEMGASAOADVGVLVISARKGEYE 377
 Db 65 AERERGKTTIDALWKFQTPEKYYTVDAGHRDFTKONMTGTSQDCAILIIAGGVGEPE 124

Qy 378 TGFPERGGOTREHALAKTOSVNRMVVSNFNLRAIGN 437
 Db 125 AGISKDGTREHALAFLIGVKQLIVAINKMD - SVKMSQDRYNEICKETANFYKVKGYN 182

Qy 438 IKTDVVFMPVSGYSGANLKDHDVDPKECPWY-----TGTPLIYLDTMMHVDRH 485
 Db 183 PKS-VFPVPSIGNGDNMIB - ASTNCDMVKGWTKLTETRAGEVKRTKLLDAIDAEPPVPR 239

Qy 486 INAPAPMPLI - AAKMDLGLTIVBEGKIESGHIGKQSTLLMPNPKTAEVQNIYNETENEVD 543
 Db 240 SDKPRLPLQDQVYKGGIGTVPGRVETVKAAGVVTPAPANTTEYKSVEMHEILPD 299

Qy 544 MAMCCEQVKLQKGVTEEDISPGFVLTSPKN - PIKSVTKFVAQIAVELKSIIAGFSCY 602
 Db 300 GGFPDNDVGFNVKQVNSVSDIRRGVYAGDSKNDPPNGCDSFNAQVYLNHPGQIGAGYAPV 359

Qy 603 MHVTAIEEVHIVLHKLEKGTRNSKSKKPPAFAKGKMKVIAVLETEAPVCVETYQDYPQ 662
 Db 360 LDCHTAHIAKCFDTLIEKIDRRTGKRMEDSPKFKSGDAIVKMPSPKMCVAFTEYPP 419

Qy 663 LGRLPFLRDQGTTIAKGKVAE 685
 Db 420 LGRPAYDRMQRQTVAG-VTKSVE 441

RESULT 12
 US-09-949-016-9570
 ; Sequence 9570, Application US/0949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: Polymorphisms in known genes associated with human disease, methods of detection and uses thereof
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768

Qy 600 SCVMHIVTVAEEHVVKLHLKLEGTNRKSRKPPAPAKGKMKVIAVLETEAPVCVETYD 659
 Db 358 APVLDCHTAHZCKFAELKEIDRSQGKCLEDGPKFLKSGDAIVDMVPGKPMCVESFD 417

Qy 660 YPQLGRFTLQDQGTTIAKGK 680
 Db 418 YPPLGRFAVDRMQRQTVAGVVI 438

PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9570
 LENGTH: 469
 TYPE: PRT
 ORGANISM: Human
 US-09-591-632-2.raii

Query Match 22.2%; Score 797.5; DB 4; Length 469;
 Best Local Similarity 38.5%; Pred. No. 2.1e-61;
 Matches 170; Conservative 88; Mismatches 158; Indels 25; Gaps 8;

Qy 258 KDHVSLIJFMGHVDAKSRSKSTMGNNLLLTGSVYDVKRTIEKRYERAKDAGRGHMYLWSWMDTNK 317
 Db 12 KTHVNIVVIGHVDSGSKSTTGHLLKCGGIDKRTIEKFEKAEGKGSFKYAWVLDKLK 71

Qy 318 EERNDGKTIIEVGKAYFETEKRYRTILDAPGHKMYSEMICGASQADGVVLVISARKGEYE 377
 Db 72 AERERGTTIDSLWKFETSKYVTTIDAPGRDFIKNMIGTQSADCALVIVAAGVGEFE 131

Qy 378 TGPERGGOTREHALAKTQGYNKMYVWNKNDPPTVNWSKERYOCVSNVSNLRAGYN 437
 Db 132 AGISONGOTREHALAYTLYGKQLLVGVNMDSTEPPYSQKRYEELVKVEYSTYIKIGYN 191

Qy 438 IKTDVYFMPVSGYSGANLKDHDVDPK-ECMPW-----TGPTLLEYLDTMINHVDR 484
 Db 192 PDT-VAFPVPSGWGDNM--LEPSANMPVFKGWVTRKDGNASTTLEADCILUPPTR 247

Qy 485 HINAPPMLPI--AAKMKDLCITIVEGKIESGHIKKGOSTLMPNKTAVEIONI--YNETEN 540
 Db 248 PTDKPURLPQDVYKIGGIPVVERETGVLPKGPNVTPAPVNTTEVKSVEMHEALS 307

Qy 541 EVDMAMCGEQVKLRLKGVEBEDISGFVLTSPKN-PIKSVTKFVAQIAVELKSIAAGF 599
 Db 308 E--ALPGDNVGENVQVSKDVRGRNVAGDSKNDPMPMEAAGFTAQVILNHPGQISAGY 364

Qy 600 SCVMVHTALEEVTIVKLHLKLEGTNRKSKKPAPAKGKMKVIAVLETEAPVCVETYQD 659
 Db 365 APVLDCHTAHACKFAELKEIDRSGKLEDGPFLSKGDAIAIVDMVPGKPMCVESFSD 424

Qy 660 YPQLGRFTLDRDQGTTIAIGK1 680
 Db 425 YPPLGRFRAVRDMDRQTVAVGVI 445

RESULT 14
 US-09-309-572-10
 ; Sequence 14
 ; Patent No. 6440730
 ; GENERAL INFORMATION:
 ; APPLICANT: Heinrich-Pette-Institut
 ; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
 ; FILE REFERENCE: P50489
 ; CURRENT APPLICATION NUMBER: US/09/309,572
 ; CURRENT FILING DATE: 1999-05-11
 ; EARLIER APPLICATION NUMBER: DE 198 56 463
 ; EARLIER FILING DATE: 1998-11-26
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: elongation factor EF-1-alpha
 ; US-09-309-572-10

Query Match 22.2%; Score 796.5; DB 4; Length 462;
 Best Local Similarity 38.3%; Pred. No. 2.5e-61;
 Matches 169; Conservative 89; Mismatches 158; Indels 25; Gaps 8;

Qy 258 KDHVSLIJFMGHVDAKSRSKSTMGNNLLLTGSVYDVKRTIEKRYERAKDAGRGHMYLWSWMDTNK 317
 5 KTHVNIVVIGHVDSGSKSTTGHLLKCGGIDKRTIEKFEKAEGKGSFKYAWVLDKLK 64

Qy 318 EERNDGKTIIEVGKAYFETEKRYRTILDAPGHKMYSEMICGASQADGVVLVISARKGEYE 377
 Db 65 AERERGTTIDSLWKFETSKYVTTIDAPGRDFIKNMIGTQSADCALVIVAAGVGEFE 124

Qy 378 TGPERGGOTREHALAKTQGYNKMYVWNKNDPPTVNWSKERYOCVSNVSNLRAGYN 437
 ; Sequence 13
 ; Patent No. 6312339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 9571
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-591-632-2.raii

RESULT 15
US-09-718-096-10
; Sequence 10, Application US/09718096
; Patent No. 6589763

GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195

CURRENT APPLICATION NUMBER: US/09/718,096
; PRIOR APPLICATION NUMBER: DE 1985663.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; OTHER INFORMATION: elongation factor EF-1-alpha
US-09-718-096-10

Query Match 22.2%; Score 796.5; DB 4; Length 462;
Best Local Similarity 38.3%; Pred. No. 2.5e-61; Indels 25; Gaps 8;
Matches 169; Conservative 89; Mismatches 158; Del 124; Gaps 124

Qy 258 KDHVSL1FMGHVDAKGSKTGTGHLTGSYDVKRTEAKDAGRCWYLSWMDTNIK 3.17
Db 5 KTHINIVVGHVDSGKSTGTGHLTAKTQGYNKMYVVNNMDPVTNWSKERYDCSVNSNFLAIGN 4.37
Qy 318 BERNDKTEVYKAYPETEKRRTYILDAPGHKMYTSEMIIGASQADGVYVISARKGEPE 3.77
Db 65 AEREGCTIDISLWKFETSKYVYTIDAPGHRDFLKNMLTGTSQADCATLIVAAVGGEPE 124
Qy 378 TGFERGQTRPHALLAKTQGYNKMYVVNNMDPVTNWSKERYDCSVNSNFLAIGN 4.37
Db 125 AGISKNGQTRPHALLAYTGLVKQLYGVNMDSTEPPYSQKRYEBIVKYSTYIKIGN 184
Qy 438 IKTDVVFMPVSGYSGANLKDQHVDPK-ECPWY-----TGTPLLEYLDTMHNVDR 4.84
Db 185 PDT-VAFVP1SGWGNM-----LEPSANMPEFGKWKTRKGOSTLMPNKTAVEQNI--YNETEN 540
Qy 485 HINAPMPLPI--AAKMKDLSITIVEKIESHIKKGOSTLMPNKTAVEQNI--YNETEN 540
Db 241 PDTKPLRPLQDVYKIGGIGTVPSRVEVGTGKPKMVVTFAPVNVTTEVSVMHEALS 300

Qy 541 EVDNAMCGEQVKURIKGVEEEDISPQFVLTSPKN-PIKSVTKEVQIAIVELKSIAGF 5.99
Db 301 E---ALPGDNVGFNWKVQKDVPRGNVAGDSNDPPMEAGTAAQVTLNHPGQISAGY 3.57
Qy 600 SCYNGHATATEEVHIVKLLHLEKGTNRKSKPPAFAKKGKMYVIAVLTBAPVCFETYOD 6.59
Db 358 APVLDCHTAIACKFAELKEIDRSGKLEDPGPFLKSGDAAIVDMVPGKPMCVESFSD 4.17
Qy 660 YPQLGRFTLBDQGTIAIGKI 6.80
Db 418 YPPGRFAVRDMRQTVAVGVI 4.38

Search completed: July 1, 2005, 18:39:39
Job time : 58.3582 secs

Result No.	Score	Query Match	Length	DB ID	Description	%
1	2549.5	70.9	662	17	US-10-732-923-17478	Sequence 17478, A
2	2367	65.9	712	17	US-10-732-923-17486	Sequence 17486, A
3	2347.5	65.3	721	14	US-10-032-885-7274	Sequence 7274, Ap
4	2283.5	63.5	701	17	US-10-732-923-17479	Sequence 17479, A
5	1877	60.6	741	17	US-10-732-923-17477	Sequence 17477, A
6	1877	52.2	742	17	US-10-732-923-17477	Sequence 17477, A
7	1679.5	46.7	690	15	US-10-369-493-22730	Sequence 22730, A
8	1658	46.1	720	15	US-10-320-797-3284	Sequence 3284, Ap
9	1626	45.2	629	15	US-10-732-923-17101	Sequence 17101, A
10	1557.5	43.3	716	14	US-10-128-714-8108	Sequence 8108, Ap
11	1519.5	42.3	712	14	US-10-128-714-3108	Sequence 3108, Ap
12	1364.5	38.0	634	15	US-10-108-260A-3174	Sequence 3174, Ap
13	1354.5	37.7	499	14	US-10-146-473-446	Sequence 46, Appl
14	1354.5	37.7	499	16	US-10-788-792-221	Sequence 231, App
15	1338.5	37.2	533	15	US-10-425-114-4453	Sequence 4453, A
16	1307.5	36.4	499	9	US-09-976-165-40	Sequence 40, Appl
17	1307.5	36.4	499	14	US-10-342-276-40	Sequence 40, Appl
18	1283.5	35.7	505	15	US-10-424-599-210116	Sequence 210116, A
19	1238	34.4	531	16	US-10-437-963-89003	Sequence 189003, A
20	1221.5	34.0	531	16	US-10-424-599-210113	Sequence 210113, A
21	1149	32.0	409	15	US-10-424-599-210113	Sequence 210113, A
22	1086	30.2	587	17	US-10-732-923-17528	Sequence 17528, A
23	1030.5	28.7	805	17	US-10-732-923-17541	Sequence 17541, A
24	1009	28.1	389	16	US-10-437-963-19100	Sequence 19100, A
25	943	26.2	600	17	US-10-732-923-17126	Sequence 17126, A
26	926.5	25.8	682	17	US-10-732-923-17127	Sequence 17127, A
27	922.5	25.7	684	17	US-10-732-923-17800	Sequence 17800, A
28	912	25.4	496	17	US-10-732-923-17799	Sequence 17799, A
29	897	25.0	652	17	US-10-732-923-17363	Sequence 17363, A
30	859.5	23.9	435	17	US-10-732-923-17119	Sequence 17119, A
31	848	23.6	653	17	US-10-732-923-17692	Sequence 17692, A
32	844	23.5	450	17	US-10-732-923-17450	Sequence 17450, A
33	844	23.5	453	17	US-10-732-923-17449	Sequence 17449, A
34	844	23.5	456	17	US-10-732-923-17451	Sequence 17451, A
35	842.5	23.4	451	17	US-10-732-923-17092	Sequence 17092, A
36	842	23.4	435	17	US-10-732-923-17086	Sequence 17086, A
37	838.5	23.3	449	17	US-10-732-923-17527	Sequence 17527, A
38	836.5	23.3	449	17	US-10-732-923-17523	Sequence 17523, A
39	829	23.1	458	17	US-10-732-923-17104	Sequence 17104, A
40	828.5	23.1	449	17	US-10-732-923-17525	Sequence 17525, A
41	828	23.0	449	17	US-10-732-923-17093	Sequence 17093, A
42	827.5	23.0	461	17	US-10-732-923-17102	Sequence 17102, A
43	826.5	23.0	434	17	US-10-732-923-17228	Sequence 17228, A
44	825.5	23.0	460	17	US-10-732-923-17111	Sequence 17111, A
45	825	23.0	458	17	US-10-732-923-17103	Sequence 17103, A
RESULT 1						
US-10-732-923-17478						
; Sequence 17478, Application US/10732923						
; Publication No. US200510891A1						
; GENERAL INFORMATION:						
; APPLICANT: Edgetech, Michael D						
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES						
; FILE REFERENCE: 38-15 (5276)C						
; CURRENT APPLICATION NUMBER: US/10/732,923						
; CURRENT FILING DATE: 2003-12-10						
; PRIOR APPLICATION NUMBER: 10/310,154						
; PRIOR FILING DATE: 2002-12-04						
; SEQ ID NO 17478						
; LENGTH: 662						
; TYPE: PRT						
; ORGANISM: Zygobaccharomyces rouxi						
US-10-732-923-17478						
Query Match 70.9%; Score 2549.5; DB 17; Length 662;						
Best Local Similarity 74.0%; Pred. No. 4.7e-157; Mismatches 53; Indels 90; Gaps 37; Gaps 15;						
; ALIGNMENTS						
QY 1 MSDSNOGNNNQNYQQYQSONGNQQGNNRNYQGY-QAYNAQAOQPAGGYQNYQGY-QYQGG 59						
Db 1 MSDPQ-NGQ-----QGGSQNAQGNSNYQQYFQKLTQOQA-QGGYQPGGGYGGT-GG 49						
; SUMMARYS						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
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Result No. Score Query Match Length DB ID Description %						
1	2549.5	70.9	662	17	US-10-732-923-17478	Sequence 17478, A
2	2367	65.9	712	17	US-10-732-923-17486	Sequence 17486, A
3	2347.5	65.3	721	14	US-10-032-885-7274	Sequence 7274, Ap
4	2283.5	63.5	701	17	US-10-732-923-17479	Sequence 17479, A
5	1877	60.6	741	17	US-10-732-923-17477	Sequence 17477, A
6	1877	52.2	742	17	US-10-732-923-17477	Sequence 17477, A
7	1679.5	46.7	690	15	US-10-369-493-22730	Sequence 22730, A
8	1658	46.1	720	15	US-10-320-797-3284	Sequence 3284, Ap
9	1626	45.2	629	15	US-10-732-923-17101	Sequence 17101, A
10	1557.5	43.3	716	14	US-10-128-714-8108	Sequence 8108, Ap
11	1519.5	42.3	712	14	US-10-128-714-3108	Sequence 3108, Ap

Qy	176 SAETK- EPTKPEKTYVEPKKEKEPKVOTEEKTEENKSELEPKVEDLKIESTHNTNNANTV 233	Db	167 ESDK- ---KEEKEKAETKEPTKEPTKV- --- --- --- -EEVKKEKEPKVOTEEKTE 207
Db	155 KKEEKAEPKEQESKEP -KREGTPRAAKDEKEKDPLKEKIKE --EQAAANAS 210	Db	194 ASKEAPKDEBAAE -PEAKKESTPVAASSPAPAAADSTPAFKKESTPPT - - - - - 245
Qy	234 SADALIKEQEEVEDEVNIDMFGKDHSVLSI FMGHDVAGKSTMGNNLLVLTGSVDKRTIE 293	Qy	208 EKSELPKVEDLKIESTHNTNNANTVTSADALIKEQEEVEDEVNIDMFGKDHSVLSI FMG 267
Db	211 GADS.LIKEQEEVEDEVNIDMFGKDHSVLSI FMGHDVAGKSTMGNNLLVLTGSVDKRTIE 270	Db	246 ---PSV- - -ASGAP/SASAVTUTADLAKEQEDDEVVVKDMFGKDHSVLSI FMG 296
Qy	294 KYERAKDAQDQGWTLISWMDTNKEERNDGKTIENGKAYFETEKRTYLLDAPGKMYVS 353	Qy	268 HVDAGKSTMGNNLLVLTGSVDKRTIEKYEREAKDAGRCWYLSWMDTNKEERNDGKTI 327
Db	271 KYERAKDAQDQGWLYISWMDTNKEERNDGKTIENGKAYFETEKRTYLLDAPGKMYVS 330	Db	297 HVDAGKSTMGNNLLVLTGSVDKRTIEKYEREAKDAGRCWYLSWMDTNKEERNDGKTI 356
Qy	354 EMIIGGASQADGVLYISARKGEYETGFERGQOTREHALAKTQGYNMVYVNNRMDPPTV 413	Qy	328 VGKAFETEGRRTYLLDAPGKMYVSEMTGASQDVGVLVISARKGEYETGFERGQOTR 387
Db	331 EMIIGGASQADGVLYISARKGEYETGFERGQOTREHALAKTQGYNL.LTINRMDPPTV 390	Db	357 VGKAFETEGRRTYLLDAPGKMYVSEMIIGGASQDVGVLVISARKGEYETGFERGQOTR 416
Qy	414 NWSKERYDOCNSVNSNFLRAIGNQKTDUVFMPVSCYSCGANLKHVDPKCPTWGPPTL 473	Qy	388 EHALLAKTQGYNKMWVYVNNRMDPPTVNSKERYDOCNSVNSNFLRAIGNQKTDUVFMPV 447
Db	391 NWSKERYDOCYKNNLSNFKALGYNKEEYVFMPPVSCYSCAGLGLTRVDPKCPTWGPALL 450	Db	417 EHALLAKTQEVNKLIIVVNAMDDPPTVNSKERYQCTTCKGVLFLGIGIN -KDDINMPV 475
Qy	474 EYLDTMNHDHINAPFMLPAIAKNDGKTIENGKAYEKGKOSTLAMPKTAIEQN 533	Qy	448 SGYSGANLKDHDPKCECPNNTGPTLLEYLDTMNHDHINAPFMLPAIAKNDGKTIENG 507
Db	451 EYMDNNSHVDKRNAAAPFMLPAIAKNDGKTIENGKAYEKGKOSTLAMPKTAIEQN 510	Db	476 SGYTAGLKDRVNPDCKPNTGPTLLEYLDTMNHDHINAPFMLPAIAKNDGKTIENG 535
Qy	534 IYNETENEVDMAMCGERQVKLRIKGVEBEDISPGFVLTSPKNPIKSUTKFWQIAVELK 593	Qy	508 KIESHSRHKQSTLIMPNTKAVATIONIYNETENEVDMAMCGERQVKLRIKGVEBEDISPGF 567
Db	511 IYNETENEVDMAMCGERQVKLRIKGVEBEDISPGFVLTSPKNPIKSUTKFWQIAVELK 570	Db	536 KIESHSRHKQSTLIMPNTKAVATIONIYNETENEVDMAMCGERQVKLRIKGVEBEDISPGF 595
Qy	594 IIAAGFSCHMVEHTAEEHVVKLRIKGVEBEDISPGFVLTSPKNPIKSUTKFWQIAVEL 653	Qy	568 VLTSKPNPIKSUTKFWQIAVELKLSIIIAAGFSCHMVEHTAEEHVVKLRIKGVEBEDISPGF 627
Db	571 ILSSEFSCHMVEHTAEEHVVKLRIKGVEBEDISPGFVLTSPKNPIKSUTKFWQIAVEL 630	Db	596 VLTSKPNPVKTVTKFWQIAVELKLSIISNGFSCHMVEHTAEEHVVKLRIKGVEBEDISPGF 655
Qy	654 VETYQDYPQLGRFLRDQGTTIAIGKIVKIAE 685	Qy	628 KSKKPPAFAKGMKVIAVLETEAPCVETYDYPQLGRFLRDQGTTIAIGKIVKIAE 683
Db	631 VETYQDYPQLGRFLRDQGTTIAIGKIVKIE 662	Db	656 KSKKPPAFAKGMKVIAVLESEPVCAETKDYDYPQLGRFLRDQGTTIAIGKIVKIAE 711
RESULT 3			
US-10-032-585-7274			
; Sequence 7274, Application US/10032555			
; Publication No. US2003018053A1			
; GENERAL INFORMATION:			
; APPLICANT: Edgerton, Michael D			
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES			
; FILE REFERENCE: 38-15 (52796)C			
; CURRENT APPLICATION NUMBER: US/10/732, 923			
; CURRENT FILING DATE: 2003-12-10			
; PRIOR APPLICATION NUMBER: US/10/310,154			
; PRIOR FILING DATE: 2002-12-04			
; NUMBER OF SEQ ID NOS: 24149			
; SEQ ID NO: 71486			
; LENGTH: 712			
; TYPE: PRT			
; ORGANISM: Candida albicans			
US-10-732-923-17486			
RESULT 2			
US-10-732-923-17486			
; Sequence 1746, Application US/10732923			
; Publication No. US2005108791A1			
; GENERAL INFORMATION:			
; APPLICANT: Edgerton, Michael D			
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES			
; FILE REFERENCE: 38-15 (52796)C			
; CURRENT APPLICATION NUMBER: US/10/732, 923			
; CURRENT FILING DATE: 2003-12-10			
; PRIOR APPLICATION NUMBER: US/10/310,154			
; PRIOR FILING DATE: 2002-12-04			
; NUMBER OF SEQ ID NOS: 24149			
; SEQ ID NO: 712			
; LENGTH: 712			
; TYPE: PRT			
; ORGANISM: Candida albicans			
US-10-732-923-17486			
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Best Local Similarity 65.9%; Score 2347.5; DB 14; Length 721;			
Matches 485; Conservative 61; Mismatches 108; Indels 62; Gaps 16;			
; US-10-032-585-7274			
Query Match			
Best Local Similarity 65.3%; Score 2347.5; DB 14; Length 721;			
Matches 471; Conservative 79; Mismatches 118; Indels 59; Gaps 17;			
; US-10-032-585-7274			
Query Match			
Best Local Similarity 64.8%; Score 2347.5; DB 14; Length 721;			
Matches 471; Conservative 79; Mismatches 118; Indels 59; Gaps 17;			
; US-10-032-585-7274			
Query Match			
Best Local Similarity 64.8%; Pred. No. 6.9E-144; Mismatches 118; Indels 59; Gaps 17;			
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; US-10-032-585-7274			
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; US-10-032-585-7274			
Query Match			
Best Local Similarity 64			

Query Match	46.11;	Score 1658;	DB 15;	Length 720;		
Best Local Matches	48.11;	Pred. No. 4.2e-99;	Mismatches 176;	Indels 88;	Gaps 13;	
Local Similarity	48.11;	Conservative	97;	Mismatches 176;	Indels 88;	Gaps 13;
Qy	38	QAPAGGYYQNYQYGSYQQGEGYQQNPNPDAGYQQQXNPFQGGYQQYQQQNFPOGG	97			
Db	48	QQQPFDPY-----GQQGGPQXG-----QIGQGQGPQYQGYGPQ-----	86			
Qy	98	RGNYKNEFVNQNLQGQA-----GFPQSQSGMSLNDFQKQQKQAAPKPKKTLKLVS	148			
Db	87	-----QGYPVPGAPGAGPRAYQP-FQARNVQGFQPSFSSPAPPDPDKAP-----	132			
Qy	149	SSGKILKA---NATKVGTKPAESDKEEERKSAETKEPTKVEEPYVCKE---KPVQ	201			
Db	133	GKPVSLSTGGGAPK---AAPSLISIEEAASSSSPPKPAAPTPKPADAPAAPKSEAASAVPS	189			
Qy	202	TEEKTEEKSELPKVEDILK-----ISERHTNNANVTS---AD	236			
Db	190	AABKKAeka---VPLTSQIGKVVAAETSAASPAKSGA-----STPVTSTSTNFSKVSAKNDAE	248			
Qy	237	ALIKEQQEEVDEVNDMFGG-----KDHYSLIENGHDAGKSTMCGNLJYLTGSYDK	289			
Db	249	AIYREQ---NLAGDAALRDLYGENVKDTNTKSHLNIIFTCHVDAAGKSTMCQGLLJYLTGAVDK	307			
Qy	290	RTEKTYEREADAGQGWYLSSWMDTNEBERNDGKTEVGKAYFETEGRTYTLDAPIHK	349			
Db	308	RTMEKTYEOKAAGRETWYLSPLADSKEERAKGKTVBVGRAYFESSECRRTYTLDAPIHK	367			
Qy	350	MYSEMIGGASQADVGVLVISARKGEYETGFERGGTREHALJAKTOGVNKVWVNQMD	409			
Db	368	TVPSMISGAAGADEVALLVLSARKGEFPTGFEBEGTYREHAMLKJNNGJNKLJTVVNQMD	427			
Qy	410	DPTVNWSKERYDOCVSNVSNFLRAIGYNTKDTDVMPYSGYSGANLXKDHVDPKCECPWYTG	469			
Db	428	DTVQNDKGRVDEBTKCTPFLKAVGPNPKDQTITPVSQAOQGENMKDRVDKXIAPWMDG	487			
Qy	470	PTLLEYLDTMNHVDRIHNAFPMLPIAAMKMDGTTVGGKIBESHHIKRGQSTLILMPNKTAV	529			
Db	488	PSLLEHLDNMEMDRNINAPMLPISEKYNELGTMWNGKIESGHVKKGDTLMMMPNKTIV	547			
Qy	530	EIONIYNETENEVDAMCGEQVKLRIKGVEERDISPGFVLTSPKNPVKSVTKEVAQIAIV	589			
Db	548	EVTFGIFSEQEDNDMAGDNTRMRISGVSDFDITPGFVLTQVKPQKAVTAKDADISI	607			
Qy	590	ELKSI1IAGFSCMVAHTAIEVHVVKLHKLEKGKTNRKSKEPPAFAKGKGMVIAVLETE	649			
Db	608	DTKVNIICPGYSCVLYHTLAEEVSVTSFLHVEKKTARKSKKPPQFAKGMVLVSALIETS	667			
Qy	650	APVCVTEVYQDYPQLGRFTLRDQGTTIAKGKIVKIAE	685			
Db	668	APICERFEDYKMLGRFTLRDEGTTVAIGKVTKLIS	703			

1 TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
 2 TITLE OF INVENTION: Methods of Use
 3 FILE REFERENCE: 10182-018-999
 4 CURRENT APPLICATION NUMBER: US/10/128,714
 5 CURRENT FILING DATE: 2002-04-23
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Db	659	FASKQQTIIARLEYVIISSAGAVCVERFEDYNQMRGFTLIRDQ	698
	RESULT 12		
	US-108-260A-3174		
	Sequence 3174, Application US/10108260A		
	Publication No. US20040005560A1		
	GENERAL INFORMATION:		
	APPLICANT: HELIX RESEARCH INSTITUTE		
	TITLE OF INVENTION: No. US20040005560A1 full length cDNA		
	FILE REFERENCE: HL-A0106		
	CURRENT APPLICATION NUMBER: US/10108260A		
	CURRENT FILING DATE: 2002-03-27		
	NUMBER OF SEQ ID NOC: 5458		
	SOFTWARE: PatentIn Ver. 2.1		
	SEQ ID NO 3174		
	LENGTH: 634		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-108-260A-3174		
Qy	Query Match	38.0%	Score 1364.5; DB 15; Length 634
Db	Best Local Similarity	49.2%	Pred. No. 4e-80; Mismatches 169; Indels 1
Qy	Matches 271; Conservative	96;	Missmatches 169; Indels 1
Qy	136 AAPPKTLKLVSSGIKLANATKVGTKPABESDKKEKEPKSAETL		
Db	91 AAPPPP-----AGCAANHAGGGAGGAAAPVSEOBESLCEB		
Qy	195 KEEPKVQEEKTEKSELPKVEDLKISETHTINANNTSADALL		
Db	145 NGTETMSPEBSWHEKEISEAEP--GGSSLGDRPPESSAHKMM		
Qy	255 FGG--KDHVSLIFPMGHVDAGKSTMGNLYLTGSVDKRTIEKYEE		
Db	202 PGAPKKEHNVVFQGHVDAGKSTIGQINLTGWDKRTIEKYEE		
Qy	313 MDTNKEERNDGKTEVKGAYFETEKKRTTILDAGCHKMYSEMIG		
Db	262 LDNTQEERDGKTVBEGRAYFETEKKRTTILDAGCHKHSVPMNIG		
Qy	373 KGEVETGPERGGTREHALAKTQGQVNAQVWVQVNDPPTVNSK		
Db	322 KGFBETGPERGGTQKEHMLAKTQGKHLIVLNIKDDPPTVNSK		
Qy	433 AIGNYKTTDVFVEMFVSGYSGANLKDHDVDPKECPWYTGPTLLEYLL		
Db	382 KVGNPKDIDHIFNFCSGLTANLQEQSD--FCPWFYGLPFIPLD		
Qy	493 PIAAKMKGKOLGTTIVEKGKIESGHIKKGQSTLMPNKTAVAEQNIYNE		
Db	440 PIYVKYKQDGTVVVLGKLESGSICKGQLYMMPNKRNVEVIGLS		
Qy	553 LRVKGKEDDISPQFVLTSPKNPITSVTKFVAQIAVLEVKSLIAP		
Db	499 IRLKGKIEEBILFGFLCDPNNLCHSGRTFDAQVWVIEKHSVII		
Qy	613 HIVKLHLEKGTRNSKSKPPAPAKGKMKVIAVLETEAPVCVTY		
Db	559 EITALICLVDKSKESKSTRPRFVQDQVCIARLRTAGTCLETH		
Qy	673 TTAIGKVKI 683		
Db	619 KTAIGKVKL 629		
Qy	RESULT 13		
Db	US-10-146-473-46		
	Sequence 46, Application US/10146473		
	Publication No. US20030108888A1		
	GENERAL INFORMATION:		
	APPLICANT: Soutan, Matthew		
	APPLICANT: Soutan, Ryan		

APPLICANT:	Stockert, Elisabeth
APPLICANT:	Gure, Ali
APPLICANT:	Chen, Yao-Tseng
APPLICANT:	Old, Lloyd
TITLE OF INVENTION:	Breast Cancer Antigens
CURRENT APPLICATION NUMBER:	US/10/146,473
CURRENT FILING DATE:	2002-05-15
PRIOR APPLICATION NUMBER:	US 60/291,150
PRIOR FILING DATE:	2001-05-15
NUMBER OF SEQ ID NOS:	82
SOFTWARE:	PatentIn version 3.0
SEQ ID NO:	46
LENGTH:	499
TYPE:	PRT
ORGANISM:	Homo sapiens
	-10-146-473-46
Query Match	37.7%
Best Local Similarity	52.5%
Matches	262;
Conservative	89;
Mismatches	139;
Indels	9;
Gaps	5;
188	KVEEEVKPVOTEKESTEKVEELKISESTHTNTNANTVSADALIKEQQEEEV 246
2	ELSEIVENGETMPEESWHKEEISEAED--GGGSLDGRPPESAHENMEEEBIP 58
247	DDEVYNDMEGG-KDHVSLIPLMGHVDAGKSTMGGNLLYLTSYDVRTIEKVYREAKDAGR 304
59	KPKSVVAPPAGPKCKHVNYYFIGHYDAKSTGQIMYLTMGWVDKTLEKTYREAKEKNR 118
305	QGWTLSWWNDTNKEERNDGKTIEVGRAYFETEKRRYTTILDAGHMKMVSMEIGGASQADV 364
119	ETWYLSWALDTNQEEERDGKGTVEGRAYFETEKGHFTILDAGHKSSTPVNMIGGASQADL 178
365	GVNIVSARKGEYETGFERGGSTREHALAKTQGVNKMVVVYVNKMDDPTVNWKERYDCV 424
179	AVLYTSARKGKFETFGKGQTREHALAKTAGVKHLLIVLNLNKMDDTVNWVNEYRBE 23.8
425	SNVSNFLRAIGYNIKTDVMPVSGYSGANJKHDVDEKECPWYTGPPILLEYDLMNHYDR 484
239	EKLVPFLKVGPNPKDIHMPMCSGQTGANLKEQSD--FCPMPYIGLPFIYLDNLPLPNFR 296
485	HINAPFMPLTAAKMQLDCTIVEGKLESGHTRKGOSTMLMPNKTAVELQNTYNETENYDM 544
297	SVGDPIRLPVYDKYKMGTVLKGLESGSICKGQOLVMMPNKHNTVTLGILSD-DVETDT 355
545	AMCQEOKVLRKIGVBEEDDISPGEVLTSPKNPKTSVTKFVAQATIVELKSITAAGFSCVMH 604
356	VAPGENLKLRLKGIBEEIILFGFILCDPNNLHSGRFDAQVIIERKSIICPGYNATH 415
605	VHTAEEVHIVKLHKLKEGTNRSKSKPPAFAKKGMRVIAVLEPAVYCQDPOLG 664
416	IHTCIEEEVITALICLVDKSGEKSCTRPREVKQDQCIAIRRTAGTICLEFKDFQMG 475
665	RFTLRDQGTIAIGKIKVI 683
476	RFTLRDGEKTAIGKVKL 494

NUMBER OF SEQ ID NOS: 254
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 231
 LENGTH: 499
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-788-792-231

Query Match 37.7%; Score 1354.5; DB 16; Length 499;
 Best Local Similarity 52.5%; Pred. No. 1..e-79; Mismatches 139; Indels 9; Gaps 5;
 Matches 262; Conservative 89; Mismatches 139; Indels 9; Gaps 5;

Qy 188 KVEEP-VKKEPKVQTEEKTEKESELPKVYEDLKLISESTHTNNNANTADALLIKEQQEEEV 246
 Db 2 ELSEPIVENGETTSEPESSWEKEEISSEAP--GGGSLYGDGRPEESAHMMEEEETP 58

Qy 247 DDEVVNDMFGG--KDHSLSJLMGHVDAKGKSTMGGLNLYLTGSYDVKRTEKYERAKDAGR 304
 Db 59 KPKSVVAPGAPKEGHVNVVFIGVDAKGSTGQIMLTMGVDKRLTEKYBRAKEKRN 11.8

Qy 305 QGWYLSQLWNTDNTKBERNDGKTIEKGAYFETEKRTTILDAPGSHKMYKSEMIGGASQADV 364
 Db 119 ETWYLSQLWALDTNQERDKRTVEGRAYFETEKRTTILDAPGHSKSFVNMGGASQADV 178

Qy 365 GVLVISARKGEYETGFERGOTREHALAKTAGYKHMVYVNNKDDPTVNSKERYDQCV 424
 Db 179 AVLVISARKGEPEKGOTEGKGGOTREHALAKTAGYKHMVYVNNKDDPTVNSKERYECK 23.8

Qy 425 SNSVNLRAIGYNIKTDVYFMPVSGYSGANLKDHDVDPKCECPWTGPTTLEYDLMNHYDR 484
 Db 239 BKLYVPFLRKVGPNPKDTHMPCSGLTGANLKEQSD--FCPWTGFLPFLPYLDNLNPNFR 29.6

Qy 485 HINAPFPLPTAAKMDLGTIVEGKIESGHIIKGOSTLMPNKTAVETQINYNETENYDM 544
 Db 297 SVDGPIRLPLVDKYKDMGTVLGLKLESGSICKRGQLVMPNPKHNEVVLGILSD-DVETDT 355

Qy 545 AMCGEQVKLRIKGVEEDISPGFVPLTSPKPNPKISVTKVQAIAVELKSIIAFGFSYMH 604
 Db 356 VAPGENKLRLKLGEEELLPGFCLCDPNLCHSGRTPDAQVIVIERSSIIICPGYNAVLH 415

Qy 605 VHTAILEVTHVKKLHKLEKGTRNRSKSKPAPAKKGMYTALEVTEAPVCVETYQDYPOLG 664
 Db 416 IHTCIEVEETALCLVDKKSGEKSRTBFRVKDQVCIARLRTAGTICLETFKDFPQMG 475

Qy 665 RFTLRDQGTTIAIGKVKI 683
 Db 476 RFTLRDGEKTTIAIGKVKL 494

RESULT 15
 US-10-425-114-44453
 Sequence 44453, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5331.3) B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 44453
 ; LENGTH: 533
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: 700963269 - FLI.pop
 ; FEATURE: US-10-425-114-44453

Query Match 37.2%; Score 1338.5; DB 15; Length 533;
 Best Local Similarity 49.4%; Pred. No. 1.6e-78; Indels 43; Gaps 7;
 Matches 263; Conservative 96; Mismatches 130; Index 7;

Qy 1512 I K L A N A T K V / G T K P A E S D K K E - E K S A E T K P K T K P T K V B E P V K K B E P K V Q T E E K T E E K S 210
 Db 39 I Q D S A E D N N G V A N A E D G R P E V E N N P D K M D D P K - - - - - Q D V A E P K A V E A P K V K D K - 91

Qy 211 E L P R V E D L K I S B E S T A N N A N V T S A D A L I R E Q E E V D E V N D M F G G D H V S L I P M G H V D 270
 Db 92 E V P S V Q D - - - - - E D E P E N T - - - - - K R H I N V V I G H V D 119

Qy 271 A G K S T M G G N L I L Y T G S V D K R T I E K Y B R E A K A D A G R Q W Y L S W M D T N K E E R N D G K T I E V G K 330
 Db 120 A G K S T G Q I U F L S G Q D V T I R T Q Y R E A K D K S R B S W Y M A T I M D T N E E R V G K T I E V G R 179

Qy 331 A Y P E T E K R Y T I L D A P G H K M Y V S E M I G G A S Q A D V G V I S A R K G E Y E T G F E R G G Q T R E H A 390
 Db 180 A H F E T T R T F T I L D A P G H K S T V P N M I S G A S Q A D V G V I S A R K G E F T G Y R E R G G Q T R E H V 239

Qy 391 L L A K T G V N R A V V V A N K M D D P T V N S K E R D Q C V S A V S N F R A I G N K I D V V F R E V S G Y 450
 Db 240 Q L A K T G V S K L L V V V N K M D E P T V Q N S K E R D I E S O M V P F L K Q S G Y N V K D V L F L P I S G L 299

Qy 451 S G A N L K D H V D P K E C P M Y G P T I L E Y D T M N H V D R H I N A P P M L P I A K M K D L G T I V E G K I E 510
 Db 300 M G A N M T R V D S V C P W N G G P L F E A D A I E P L R D E N G P F M P I D K F R D G T V M G K V E 359

Qy 511 S G H I K K G Q S T I L M P N K T A V E L O N I N Y E T E N V D M A M C G E Q Y K L R I K G V E E D I S P G F V L T 570
 Db 360 S G S V R E G D S I L V M P N K D P V K V A I F D - E D R V K A R G P G E N I R I L S G V E E B D I L S G F V L S 418

Qy 571 S P R N P I K S V T R E V A Q I A V E L - K S T I A A G S C V M R H T A E E V H I V R L L H R L E B G T N R K 628
 Db 419 S V A N P P P A V T E F V A Q L V I L L D N A L F T A G Y K A V L H I H S V V E C E V E L L Q Q I D T K T K C P 478

Qy 629 S K K P P A F A K K M K V I A V L E T E A P C V T E Y D P O L G R F T L R D O G T I A I G K I 680
 Db 479 M K K R V I L F V R N G A V V V Q V N N S I C I E K S D F P Q L G R F T L R T E G K I V A V G K V 530

Search completed: July 1, 2005, 18:44:19
 Job time : 183.127 sec

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